



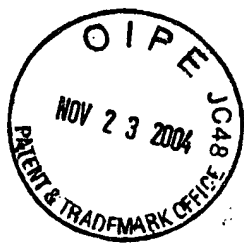
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10	20	30	40	50	60
MALAGAPAG	PCAPALEALL	GAGALRLDS	SQIVIISAAQ	DASAPPAPTG	PAAPAAAGPCD
70	80	90	100	110	120
POLLLEFATPQ	APRPTPSAPR	PALGRPPVKR	RLDLETDHQY	LAESSGPARG	RGRHPGKGVK
130	140	150	160	170	180
SPGEKSRYET	SLNLTTKREF	ELLSHSADGV	VDLNWAAEVL	KVQKRRIYDI	TNVLEGIQLI
190	200	210	220	230	240
AKKSKNHIQW	LGSHTTWGVG	GRLEGLTQDL	RQLQESEQQL	DHLMNICTTQ	LRLLEDTS
250	260	270	280	290	300
ORLAYVTCQD	LRSIADPAEQ	MVMVIKAPPE	TQLQAVDSSE	NFQISLKSQ	GPIDVFLCPE
310	320	330	340	350	360
ETVGGISPCK	TPSQEVTSEE	ENRATDSATI	VSPPPSSPPS	SLTTDPSQSL	LSLEQEPLLS
370	380	390	400	410	420
RMGSLRAPVD	EDRLSPLVAA	DSLLEHVRED	FSGLLPEEFI	SLSPPEALD	YHFGLEEGEG
430	440	450	460	470	480
IRDLFDCDEG	DLTPLDF*	.....	.....	.....	.....

FIG. 1A.



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10 20 30 40 50 60  
GGAATTCCGT GGCCGGGACT TTGCAGGCAG CGGCGGCCCG GGGCGGAGCG GGATCGAGCC  
70 80 90 100 110 120  
CTCGCCGAGG CCTGCCGCCA TGGGCCCGCG CCGCCGCCGC CGCCTGTAC CCGGGCCGCG  
130 140 150 160 170 180  
CGGGCCGTGA GCGTCATGEC CTTGGCCGGG GCCCCCTGCG GCGGCCCATG CGCGCCGCGG  
190 200 210 220 230 240  
CTGGAGGCC TGCTCGGGC CGGCGCGCTG CCGCTGCTCG ACTCCTCGCA GATCGTCATC  
250 260 270 280 290 300  
ATCTCCGCG CGCAGGACGC CAGCGCCCCG CCGGCTCCCA CCGGCCCGC GCGGCCCGCC  
310 320 330 340 350 360  
GCCGGCCCT GCGACCCTGA CCTGCTGCTC TTCGCCACAC CGCAGGCGCC CCGGCCACA  
370 380 390 400 410 420  
CCCAGTGGC CGCGGCCCGC GCTCGGCCG CCGCCGTGA AGCGGAGGCT GGACCTGGAA  
430 440 450 460 470 480  
ACTGACCATC AGTACCTGGC CGAGAGCAGT GGGCCAGETC GGGCAGAGG CCGCCATCCA  
490 500 510 520 530 540  
GGAAAAGTG TGAATCCCC GGGGAGAAG TCACGCTATG AGACCTCACT GAATCTGACC  
550 560 570 580 590 600  
ACCAAGCGT TCCTGGAGCT GCTGAGCCAC TCGGCTGACG GTGTCGTGGA CCTGAAGTGG  
610 620 630 640 650 660  
GCTGCCGAG TGCTGAAGT GCAGAAGCG CGCATCTATG ACATCACCAA CGTCCTTGAG

FIG 1B-1.



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670 GGCATCCAGC 680 TCATTGCCAA 690 GAAGTCCAAG 700 AACACATCC 710 AGTGGCTGGG 720 CAGCCACACC  
730 ACAGTGGCG 740 TCGGCGGACG 750 GCTTGAGGGG 760 TTGACCCAGG 770 ACCTCCGACA 780 GCTGCAGGAG  
790 AGCGAGCAGC 800 AGCTGGACCA 810 CCTGATGAAT 820 ATCTGTACTA 830 CGCAGCTGCG 840 CCTGCTCTCC  
850 GAGGACACTG 860 ACAGCCACCG 870 CCTGGCCTAC 880 GTGACGTGTC 890 AGGACCTTCG 900 TAGCATTGCA  
910 GACCCCTGCAG 920 AGCAGATGGT 930 TATGGTGATC 940 AAAGCCCCCTC 950 CTGAGACCCA 960 GCTCCAAGCC  
970 GTGGACTCTT 980 CGGAGAACTT 990 TCAGATCTCC 1000 CTTAAGAGCA 1010 AACAAGGCC 1020 GATCGATGTT  
1030 TTCCCTGTGCC 1040 CTGAGGAGAC 1050 CGTAGGTGGG 1060 ATCAGCCCCTG 1070 GGAAGACCCC 1080 ATCCCAGGAG  
1090 GTCACCTTCTG 1100 AGGAGGAGAA 1110 CAGGGCCACT 1120 GACTCTGCCA 1130 CCATAGTGC 1140 ACCACCACCA  
1150 TCATCTCCCC 1160 CCTCATCCCT 1170 CACCACAGAT 1180 CCCAGCCAGT 1190 CTCTACTCAG 1200 CCTGGAGCAA  
1210 GAACCGCTGT 1220 TGTCCCGGAT 1230 GGCAGCCCTG 1240 CCGGCTCCCG 1250 TGGACGAGGA 1260 CCGCCTGTCC

FIG. 1B-2.



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1270 1280 1290 1300 1310 1320  
CCGCTGGTGG CGCCGACTC GCTCCTGGAG CATGTGCGGG AGGACTTCTC CGGCCCTCCTC  
1330 1340 1350 1360 1370 1380  
CCTGAGGAGT TCATCAGCCT TTCCCCACCC CACGAGGCC TCGACTACCA CTTCGGCCTC  
1390 1400 1410 1420 1430 1440  
GAGGAGGGCG AGGGCATCAG AGACCTCTTC GACTGTGACT TTGGGGACCT CACCCCCCTG  
1450 1460 1470 1480 1490 1500  
GATTCTCTGAC AGGGCTTGA GGGACCAGGG TTTCCAGAGT AGCTCACCTT GTCTCTGCAG  
1510 1520 1530 1540 1550 1560  
CCCTGGAGCC CCCTGTCCCT GGCCGTCCTC CCAGCCTGTT TGGAAACATT TAATTATAC  
1570 1580 1590 1600 1610 1620  
CCCTCTCCTC TGTCTCCAGA AGCTTCTAGC TCTGGGGTCT GGCTACCGCT AGGAGGCTGA  
1630 1640 1650 1660 1670 1680  
GCAAGCCAGG AAGGAAGGA GTCTGTGTGG TGTGTATGT CATGCAGCCT ACACCCACAC  
1690 1700 1710 1720 1730 1740  
GTGTGTACCG GGGGTGAATG TGTGTGAGCA TGTGTGTGTG CATGTACCGG GGAATGAAGG  
1750 1760 1770 1780 1790 1800  
TGAACATACA CCTCTGTGTG TGCACCTGCAG ACACGCCCCA GTGTGTCCAC ATGTGTGTGC  
1810 1820 1830 1840 1850 1860  
ATGAGTCCAT CTCTGCGCGT GGGGGGGCTC TAACTGCACT TTGGGCCCTT TTGCTCGTGG  
1870 1880 1890 1900 1910 1920  
GGTCCCACAA GGCCAGGGC AGTGCCCTGCT CCCAGAATCT GGTGCTCTGA CCAGGCCAGG

FIG. 1B-3.

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1930	1940	1950	1960	1970	1980
TGGGGAGGCT	TTGGCTGGCT	GGGCGTGTAG	GACGGTGAGA	GCACTTCTGT	CTTAAAGGTT
1990	2000	2010	2020	2030	2040
TTTCTCTGATT	GAAGCTTTAA	TGGAGCGTTA	TTTATTATC	GAGCCCTCTT	TGGTGAGCCT
2050	2060	2070	2080	2090	2100
GGGGAATCAG	CAAAAGGGA	GGAGGGGTGT	GGGGTTGATA	CCCCAACTCC	CTCTACCCCT
2110	2120	2130	2140	2150	2160
GAGCAAGGC	AGGGTCCCT	GAGCTGTCT	TCTGCCCAT	ACTGAAGGA	CTGAGGCCCTG
2170	2180	2190	2200	2210	2220
GGTGATTAT	TTATTGGGA	AGTGAGGGAG	GGAGACAGAC	TGACTGACAG	CCATGGGTGG
2230	2240	2250	2260	2270	2280
TCAGATGGTG	GGGTGGCCC	TCTCCAGGG	GCCAGTTCAG	GGCCCCAGCTG	CCCCCCAGGA
2290	2300	2310	2320	2330	2340
TGGATATGAG	ATGGGAGAGG	TGAGTGGGG	ACCTTCACTG	ATGTGGGCAG	GAGGGGTGGT
2350	2360	2370	2380	2390	2400
GAAGGCCCTCC	CCCAGCCCAG	ACCCGTGTGT	CCCTCCTGCA	GTGTCTGAAG	CGCCTGCCCTC
2410	2420	2430	2440	2450	2460
CCCACTGCTC	TGCCCCACCC	TCCAATCTGC	ACTTTGATT	GCTTCCTAAC	AGCTCTGTTC
2470	2480	2490	2500	2520	2520
CCTCCTGCTT	TGGTTTAAAT	AAATATTTTG	ATGACGTTAA	AAAAAGGAAT	TCGATAT

FIG. 1B-4.

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1 tccgggtttt tctcagggga cgttgaaatt atttttgtaa cgggagtcgg gagaggacgg  
61 ggcggtgccc gcgtgcgcgc gcgtgcctt cccggcgct cctccacagc tcgctggctc  
121 ccgccgcgga aagcggtcat gccgcccaga acccccga accggccgc caccgccc  
181 gctgcccgcg cggaaacccc gcccgagga cctgcctctc gcaggccttg agttgaaga aacagaagaa  
241 caggacagcg cctgatttta ctgcattatg tcagaaatta ttcattcttg gatgagttat tttcaaaa  
301 cctgatttta cctgattatg gcgagaaagt ttcattcttg gatgagttat tttcaaaa  
361 tgggttaactt gggagaaagt ttcattcttg gatgagttat tttcaaaa  
421 aaaaaggaaac tgggggaat ctgtatcttt gaaatacagt gataatgcta tgcacaagct gttgaagaag  
481 ttcactttta ctgagctaca gaaaacata taccagaaat cttcagcaaa atactactga taaaggga gttccttgac  
541 ctaaaagaaa ttgataccag ttttgcac atctactga taaaggga gttccttgac ttttatta cccattaatg  
601 tatgatgtat ttttgcac atctactga taaaggga gttccttgac ttttatta cccattaatg gttcacctcg  
661 acacaaccca ttttgcac atctactga taaaggga gttccttgac ttttatta cccattaatg gttcacctcg  
721 tggatcacat ttttgcac atctactga taaaggga gttccttgac ttttatta cccattaatg gttcacctcg  
781 tcatctcagt taatgctatg taatgctatg taatgctatg taatgctatg taatgctatg taatgctatg taatgctatg  
841 ctcaagaac catataaaac agctgttata cccattaatg gttcacctcg aacacccagg aagaattatt  
901 cgaggtcaga acagagtgac acggtatgca aacacactag aagaattatt ttaattcaaa  
961 gaagttctct gtaagaaca tgaatgtaat atagatgagg tgaataatgt ttaattcaaa  
1021 aattttatc cttttatgaa ttctcttgga cttgtaacat ctaattggact tccagaggtt  
1081 gaaaatcttt ctcaacgata cgaagaaatt tatcttaaaa ataaagatct agatgcaaga  
1141 ttttttttg atcatgataa aactcttcag actgattcta tagacagttt tgaacacag  
1201 agaacaccac gaaaagtaa ccttgatgaa gaggtgaatg taattcctcc acacactcca  
1261 gtaggactg tttgaacac tatccaaca ttaatgatga ttttaaatc agcaagtga  
1321 caaccttcag aaaactgat ttcctatttt aacaactgca cagtgaatcc aaaagaaagt  
1381 atactgaaaa gagtgaaggaa tataggatac atctttaaa agaaatttgc taaagctgtg  
1441 ggacagggtt gtgtcgaat tggatcacag cgatacaaac ttggagttcg cttgtattac

FIG. 2A-1.



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1501 cgagtaattg aatccatgct taaccagaa gaagaacgat tatccattca aaatttttagc  
1561 aaacttctga atgacaacat ttttcatatg tctttattgg cgtgcgctct tgaggtttgta  
1621 atggccacat atagcagaag tacatctcag aatcttgatt ctggaacaga tttgtcttttc  
1681 ccatggattc tgaatgtgct taatttaaa gcctttgatt ttacaaaagt gatcgaaagt  
1741 tttatcaaa cagaaggcga ctgacaaga tgcattggctc tcaatttga aacatttga acgatgtgaa  
1801 catcgaatca tggaaatcct accgagaag ataatacac caactacgcg tgtaaatctt ctttatttga tcttatttaa  
1861 caatcaaagg accgagaag caactacac caactacgcg tgtaaatctt ctttatttga tcttatttaa  
1921 cctctccaga ataatacac caactacgcg tgtaaatctt ctttatttga tcttatttaa  
1981 aaaaaagggt caactacgcg tgtaaatctt ctttatttga tcttatttaa  
2041 gccttccaga cccagaagcc attgaaatct gctaaataca ctttatttga tcttatttaa  
2101 tatcggctag cctatctcgc gctaaataca ctttatttga tcttatttaa  
2161 gaattagaac atatactctg gacccctttc cagcacacc atgtgttcca gtaacagcat acaaggatct tcttatttga  
2221 atgagagaca ggcatttggg ccaaatctt ccaaatctt gtaacagcat acaaggatct tcttatttga  
2281 aagaatatag accttaaat cattcaaac cgttcttcat gcagagactg aaacaaata attcctcgaa gcttatttga  
2341 gttcaggaga ctttcaaac cgttcttcat gcagagactg aaacaaata attcctcgaa gcttatttga  
2401 tcttataact cgttcttcat gcagagactg aaacaaata attcctcgaa gcttatttga  
2461 agggccctta ccttctcacc aggttctcgc ggccttataa ggccttataa ggccttataa  
2521 tcaccccttac ggccttctgc ggccttataa ggccttataa ggccttataa ggccttataa  
2581 atttcagaag ggccttctgc ggccttataa ggccttataa ggccttataa ggccttataa  
2641 atttggtgaat cattcgggac tcttgagaag tcttgagaag tcttgagaag tcttgagaag  
2701 agcgaccgtg tgcctcaaaag aagtgcgtga ggccttataa ggccttataa ggccttataa  
2761 ctacgctttg atattgaag atcagatgaa ggccttataa ggccttataa ggccttataa  
2821 tccaaatttc agcagaact ggcagaaatg acttctactc ggcagaaatg acttctactc  
2881 aaaatgaatg atagcatgga tacctcaaac aaggaagaga aatgaggatc agatgtgact  
2941 ggtggacact gtgtacacct ctggattcat tgcctctcac agatgtgact

FIG 2A-2.



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"MPPKTPRKTAATAAAAEPPAPPPPEEDPEQDSGPEDLPL  
VRLEFEETEEDFTALCQKLKIPDHVRERAWLTWEKVSSVDGLGGYIQKKKELWGIC  
IFIAAVDLDEMSFTTELOKNIEISVHKFFNLLKEIDTSTKVDNAMSRLKKYDVLFA  
LFSKLERTECELIYLTQPSSEISTEINSALVLKVSWITFLAKGEVLQMEDDLVISFQL  
MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPTPRRGQNRSARIAKQLENDTRIIEV  
LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLNKNDLDAR  
LFLDHDKTLQTDSDSFETQRTPRKSNLDEEVNVIPPHTPVRTVMNTIQQLMMILNSA  
SDQPSENLISYFNNTVNPKEISILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLG  
RLYRVMESMLKSEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDS  
GTDLSFPWILNVNLKAFDFYKVIESFIKAEGNLTREMIXHLERCEHRIMESLAWLSD  
SPLFDLIKQSKDREGPTDHLKSTSLFYKKVYRLAYLRNLTLCEERLLSEHPELEHIIWT  
TANAETQATSAFQTKPLKSTSLFYKKVYRLAYLRNLTLCEERLLSEHPELEHIIWT  
LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK  
RVLIKEEYDSIIIVFVNSVFMORLKNILQYASTRPPPTLSPIPHIPRSPYKFPSSPLR  
IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSI GSEGTSEKFQKINQMVCNSD  
RVLKRS AEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQLAEMTSTRTRMQKQ  
KMND SMDTSNKEEK"

FIG 2B.





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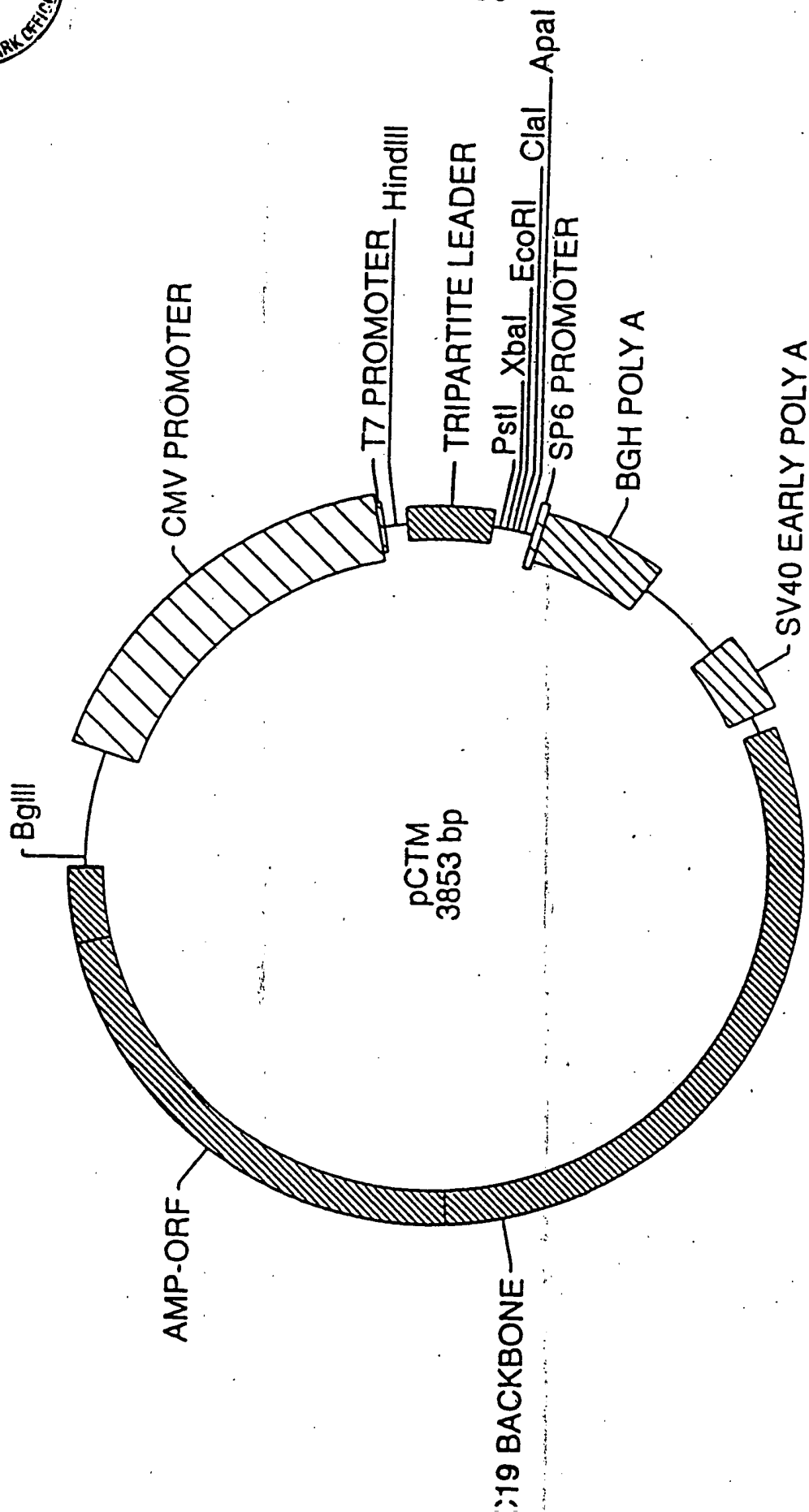


FIG. 3.

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**FIG. 4-1.**

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>AatII
|
430
| *
TCA ATG GGT GGA CTA TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA
Ser Met Gly Gly Leu Phe Thr Val Asn Cys Pro Leu Gly Ser Thr Ser>
d d d d d CMV PROMOTER d d d d d
|
440
| *
450
| *
460
| *
470
|
>BglI

>NdeI
|
480
| *
490
| *
500
| *
510
| *
520
|
AGT GTA TCA TAT GCC AAG TAC GCC CCC TAT TGA CGT CAA TGA CGG TAA
Ser Val Ser Tyr Ala Lys Tyr Ala Pro Tyr *** Arg Gln *** Arg ***>
d d d d d CMV PROMOTER d d d d d
|
>BglI
|
530
| *
540
| *
550
| *
560
| *
570
|
ATG GCC CGC CTG GCA TTA TGC CCA GTA CAT GAC CTT ATG GGA CTT TCC
Met Ala Arg Leu Ala Leu Cys Pro Val His Asp Leu Met Gly Leu Ser>
d d d d d CMV PROMOTER d d d d d
|
>BsaAI
|
580
| *
590
| *
600
| *
610
|
TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT
Tyr Leu Ala Val His Leu Arg Ile Ser His Arg Tyr Tyr His Gly Asp>
d d d d d CMV PROMOTER d d d d d
|
>NcoI
|
>StyI
|
>MslI
|

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FIG 4-3.



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620      *      630      640      650      660
      *      *      *      *      *
      GGT TTG GCA GTA CAT CAA TGG GCG TGG ATA GCG GTT TGA CTC ACG
      Ala Val Leu Ala Val His Gln Trp Ala Trp Ile Ala Val *** Leu Thr>
      d_d_d_d_d_d_CMV PROMOTER_d_d_d_d_d_d_>

      >AatII      >BamI
      670      680      690      700      710
      *      *      *      *      *
      GGT ATT TCC AAG TCT CCA CCC CAT TGA CGT CAA TGG GAG TTT GTT TTG
      Gly Ile Ser Lys Ser Pro Pro His *** Arg Gln Trp Glu Phe Val Leu>
      d_d_d_d_d_d_CMV PROMOTER_d_d_d_d_d_d_>

      720      730      740      750      760
      *      *      *      *      *
      GCA CCA AAA TCA ACG GGA CTT TCC AAA ATG TCG TAA CAA CTC CGC CCC
      Ala Pro Lys Ser Thr Gly Leu Ser Lys Met Ser *** Gln Leu Arg Pro>
      d_d_d_d_d_d_CMV PROMOTER_d_d_d_d_d_d_-d_->

      770      780      790      800      810
      *      *      *      *      *
      ATT GAC GCA AAT GGG CCG TAG GCG TGT ACG GTG GGA GGT CTA TAT AAG
      Ile Asp Ala Asn Gly Arg *** Ala Cys Thr Val Gly Gly Leu Tyr Lys>
      d_d_d_d_d_d_CMV PROMOTER_d_d_d_d_d_d_>

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FIG. 4-4.

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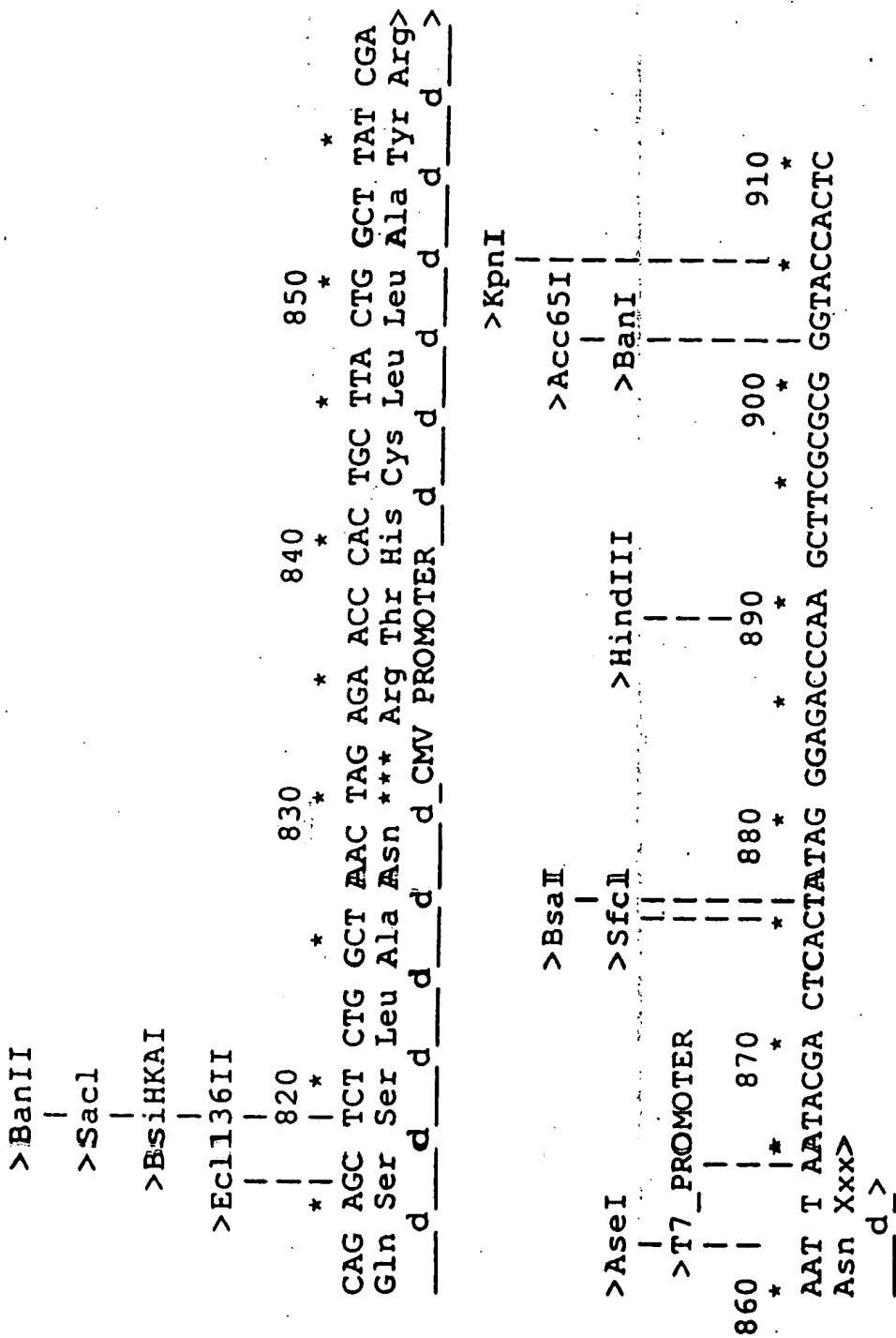


FIG. 4-5.

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**FIG. 4-7.**





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>Bani  
|  
1210 \* 1220 \* 1230 \* 1240 \* 1250 \* 1260 \*  
GTTGTTGCC CCTCCCCCGT GCCTTCCTTG ACCCTGGAAG GTGCCACTCC CACTGTCCCTT  
1270 \* 1280 \* 1290 \* 1300 \* 1310 \* 1320 \*  
TCCTAATAA ATGAGGAAAT TGCATCGCAT TGTCTGAGTA GGTGTCATTC TATTCTGGGG

>BbsI  
|  
1330 \* 1340 \* 1350 \* 1360 \* 1370 \* 1380 \*  
GGTGGGGTGG GGCAGGACAG CAAGGGGAG GATTGGGAAG ACAATAGCCG AAATGACCGA

>BssSI  
|  
>BspMI  
|  
1390 \* 1400 \* 1410 \* 1420 \* 1430 \* 1440 \*  
CCAAGCGAG CCCAACCTGC CATCAGGAGA TTTCGATTCC ACCGCCGCCT TCTATGAAAG

>NaeI  
|  
>BsrFI  
|  
>BpmI  
|  
>NgOMI  
|  
1450 \* 1460 \* 1470 \* 1480 \* 1490 \* 1500 \*  
GTTGGGCTTC GGAATCGTTT TCCGGGACGC CGGCTGGATG ATCCTCCAGC GCGGGGATCT

G.4-8.



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>BpmI  
|  
>SV40\_early\_poly\_A  
|  
1510 \* 1520 \* 1530 \* 1540 \* 1550 \* 1560 \*  
CATGCTGGAG TTCTTCGCCC ACCCCAACCT GTTTATTGCA GCTTATAATG GTTACAAATA  
|  
>ApoI  
|  
1570 \* 1580 \* 1590 \* 1600 \* 1610 \* 1620 \*  
AAGCAATAGC ATCACAATTT TCACAAATAA AGCATTTTTT TCACTGCATT CTAGTTGTGG  
|  
>BsmI  
|  
>HincII  
|  
>Bst1107I >AccI  
|  
>AccI >SalI  
|  
1630 \* 1640 \* 1650 \* 1660 \* 1670 \* 1680 \*  
TTTGTCCAA CTCATCAATG TATCTTATCA TGTCTGTATA CCGTCGACCT CTAGCTAGAG  
|  
>BsrBI  
|  
1690 \* 1700 \* 1710 \* 1720 \* 1730 \* 1740 \*  
CTTGGCGTAA TCATGGTCAT AGCTGTTTCC TGTGTGAAAT TGTATCCGC TCACAATTCC  
|  
c PUC19 BACKBONE H3 TO AATII c

FIG. 4-9.



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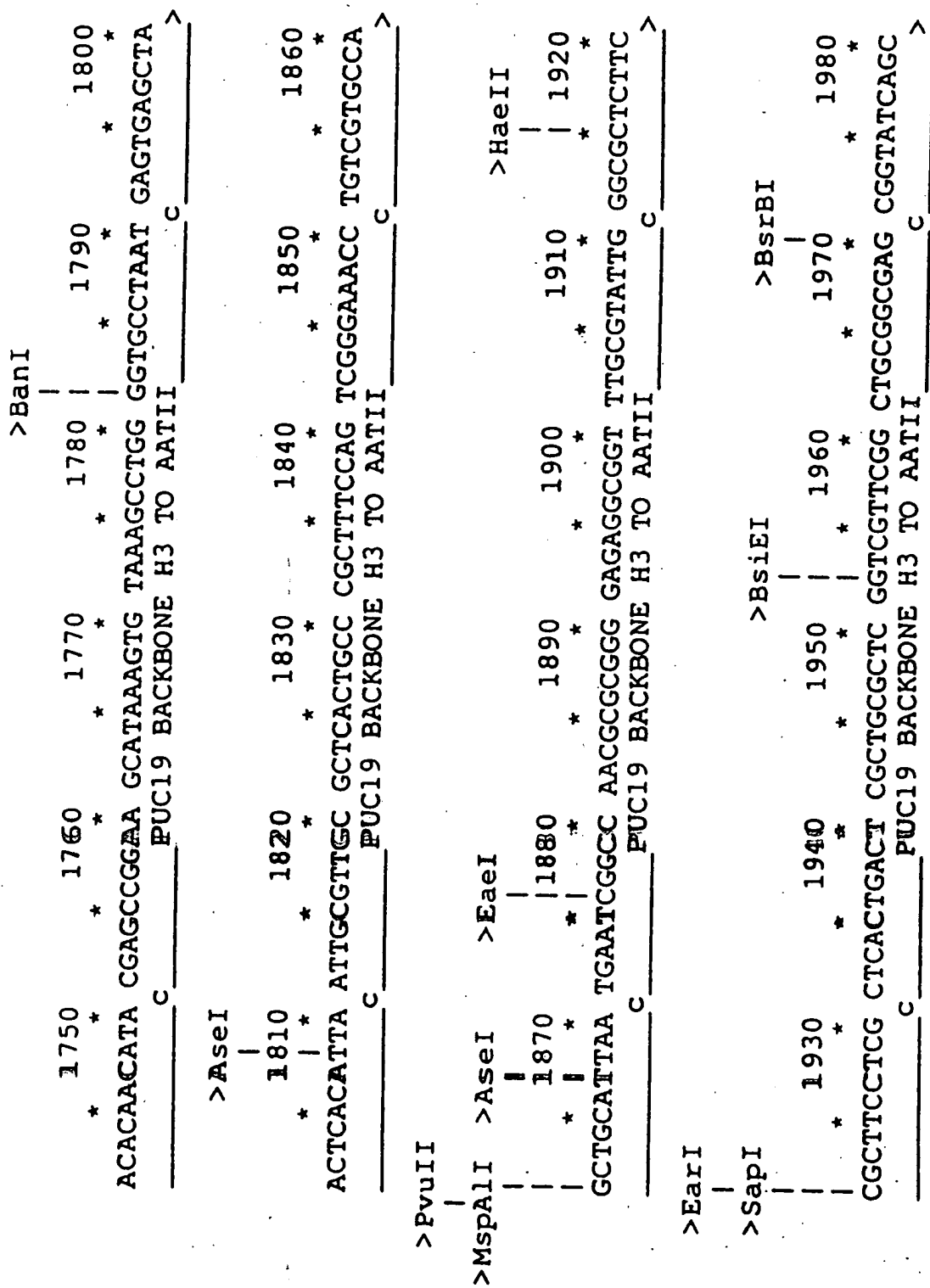


FIG. 4-10.

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>AflIII  
1990 2000 2010 2020 2030 2040  
\* \* \* \* \*  
TCACTCAAAG GCGGTAATAC GGTATCCAC AGAATCAGGG GATAACGCAG GAAAGAACAT  
c PUC19 BACKBONE H3 TO AATII c  
2050 2060 2070 2080 2090 2100  
\* \* \* \* \*  
GTGAGCAAAA GGCCAGCAAA AGGCCAGGAA CCGTAAAAAG GCCGCGTTGC TGGCGTTTT  
c PUC19 BACKBONE H3 TO AATII c  
>  
>DrdI  
2110 2120 2130 2140 2150 2160  
\* \* \* \* \*  
CCATAGGCTC CGCCCCCTG ACGAGCATCA CAAAATCGA CGCTCAAGTC AGAGGTGGCG  
c PUC19 BACKBONE H3 TO AATII c  
>  
>BsSSI  
2170 2180 2190 2200 2210 2220  
\* \* \* \* \*  
AAACCCGACA GGAATATAAA GATACCAGGC GTTCCCCCT GGAAGCTCCC TCGTGGCGTC  
c PUC19 BACKBONE H3 TO AATII c  
>  
>BsawI  
2230 2240 2250 2260 2270 2280  
\* \* \* \* \*  
TCCTGTTCGG ACCCTGCCGC TTACCGGATA CCTGTCCGCC TTTCTCCCTT CGGGAAGCGT  
c PUC19 BACKBONE H3 TO AATII c  
>

FIG 4-11.

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>HaeII          >SfcI
|              |
| 2290          | 2300 | 2310
*              *      *
GGCGCTTTCT CAATGCTCAC GCTGTAGGTA TCTCAGTTTCG GTGTAGGTCG TTGGCTCCAA
      C          PUC19 BACKBONE H3 TO AATII C
>BsiHKAI          >MspAI
|              |
| 2350          | 2360          | 2370          | 2380          | 2390          | 2400
*              *      *      *      *      *
GCTGGGCTGT GTGCACGAAC CCCCCGTTCA GCCCGACCGC TGGCCCTTAT CCGGTAACATA
      C          PUC19 BACKBONE H3 TO AATII C
>AlwNI
|              |
| 2410          | 2420          | 2430          | 2440          | 2450          | 2460
*              *      *      *      *      *
TCGTCTTGAG TCCAACCCGG TAAGACACGA CTTATCGCCA CTGGCAGCAG CCACTGGTAA
      C          PUC19 BACKBONE H3 TO AATII C
>SfcI
|              |
| 2470          | 2480          | 2490          | 2500          | 2510          | 2520
*              *      *      *      *      *
CAGGATTAGC AGAGCGAGGT ATGTAGGCGG TGCTACAGAG TTCTTGAAGT GGTGGCCTAA
      C          PUC19 BACKBONE H3 TO AATII C
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FIG. 4-12.

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2530 \* 2540 \* 2550 \* 2560 \* 2570 \* 2580 \*  
CTACGGCTAC ACTAGAAGGA CAGTATTGG TATCTGGCT CTGCTGAAGC CAGTTACCTT  
C PUC19 BACKBONE H3 TO AATII C >

>Eco57I

>MspAI

2590 \* 2600 \* 2610 \* 2620 \* 2630 \* 2640 \*  
CGGAAAAAGA GTTGGTAGCT CTTGATCCGG CAAACAAACC ACCGCTGGTA GCGGTGGTTT  
C PUC19 BACKBONE H3 TO AATII C >

2650 \* 2660 \* 2670 \* 2680 \* 2690 \* 2700 \*  
TTTTGTTGC AAGCAGCAGA TTACGGGCAG AAAAAAGGA TCTCAAGAAG ATCCTTTGAT  
C PUC19 BACKBONE H3 TO AATII C >

>BspHI

2710 \* 2720 \* 2730 \* 2740 \* 2750 \* 2760 \*  
CTTTCTACG GGGCTGACG CTCAGTGGAA CGAAACTCA CGTTAAGGA TTTTGGTCAT  
C PUC19 BACKBONE H3 TO AATII C >

>DraI

>DraI

2770 \* 2780 \* 2790 \* 2800 \* 2810 \* 2820 \*  
GAGATTATCA AAAAGGATCT TCACCTAGAT CCTTTAAAT TAAAAATGAA GTTTTAAATC  
C PUC19 BACKBONE H3 TO AATII C >

FIG 4-13.

+

**FIG. 4-14.**



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>AseI  
3070 \* 3080 \* 3090 \* 3100 \* 3110 \* 3120 \*  
CAGAAGTGGT CCTGCAACTT TATCCGCCCTC CATCCAGTCT ATTAATTGTT GCCGGGAAGC  
a c PUC19 BACKBONE H3 TO AATII a c

>PspI406I

>FspI | >BsrDI | >Sfcl  
3130 \* 3140 \* 3150 \* 3160 \* 3170 \* 3180 \*  
TAGAGTAAGT AGTTCGCCAG TTAATAGTTT GCGCAACGTT GTTGCCATTG CTACAGGCAT  
a c PUC19 BACKBONE H3 TO AATII a c

>MslI

>BsaWI  
3190 \* 3200 \* 3210 \* 3220 \* 3230 \* 3240 \*  
CGTGGTGTC A CGCTCGTCGT TTGGTATGGC TTCATTACGC TCCGGTTCCC AACGATCAAG  
a c PUC19 BACKBONE H3 TO AATII a c

FIG. 4-15.

+





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>PvuI  
|  
>BsiEI

3250 \* 3260 3270 3280 3290 3300  
\* \* \* \* \*  
GCGAGTTACA TGATCCCCCA TGTGTGCAA AAAAGCGGTT AGTCCTCTCG GTCCTCCGAT  
a a a a a  
c c PUC19 BACKBONE H3 TO AATII a c

>EaeI  
|  
>MslI

3310 3320 3330 3340 3350 3360  
\* \* \* \* \*  
CGTTGTCAGA AGTAAGTTGG CCGCAGTGT ATCACTCATG GTTATGGCAG CACTGCATAA  
a a a a a  
c c PUC19 BACKBONE H3 TO AATII a c

>ScaI  
|

3370 3380 3390 3400 3410 3420  
\* \* \* \* \*  
TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTCTGTG ACTIGGTGAGT ACTCAACCAA  
a a a a a  
c c PUC19 BACKBONE H3 TO AATII a c

>BsiEI  
|

3430 3440 3450 3460 3470 3480  
\* \* \* \* \*  
GTCATTCTGA GAATAGTGTA TCGGGCGACC GAGTTGCTCT TGCCCGGCGT CAATACGGGA  
a a a a a  
c c PUC19 BACKBONE H3 TO AATII a c

G.4-16.



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>XmnI  
|  
>PspI406I  
|  
>DraI >BsiHKAI  
| 3510 | 3520 | 3530 | 3540  
\* \* \* \* \*  
TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG  
a a AMP-ORF a  
c PUC19 BACKBONE H3 TO AATII c

>Eco57I  
|  
>ApaLI  
|  
>BssSI  
| 3590 | 3600  
\* \* \* \* \*  
GCGAAAAC TC AAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGTGC  
a a AMP-ORF a  
c PUC19 BACKBONE H3 TO AATII c

>BsiHKAI  
| 3610 | 3620 | 3630 | 3640 | 3650 | 3660  
\* \* \* \* \*  
ACCCAAC TGA TCTTCAGCAT CTTTACTTT CACCAGCGTT TCTGGGTGAG CAAAACAGG  
a a AMP-ORF a  
c PUC19 BACKBONE H3 TO AATII c

FIG. 4-17.



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+

```
>MslI
3670      *      3680      3690      3700      3710      3720
*      *      *      *      *      *      *
AAGGCAAAAT GCCGCAAAA AGGGAATAAG GCGACACGG AATGTTGAA TACTCATACT
a      a      AMP-ORF
c      c      PUC19 BACKBONE H3 TO AATII a      c      >

>EarI      >SspI      >BspHI      >BsrBI
|      |      |      |
| 3730      | 3740      3750      3760      | 3770      | 3780
*      *      *      *      *      *      *
CTTCCTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT TGTCTCATGA GCGGATACAT
c      c      PUC19 BACKBONE H3 TO AATII c      c      >

3790      *      3800      3810      3820      3830      3840
*      *      *      *      *      *      *
ATTGAATGT ATTAGAAAA ATAACAAT AGGGGTTCCG CGCACATTTC CCCGAAAAGT
c      c      PUC19 BACKBONE H3 TO AATII c      c      >

>HincII
|
>AccI
||
>AatII
||
>SalI
|||
3850      *      |||
*      *      |||
GCCACCTGAC GTC
c      c      >
```

FIG 4-18.

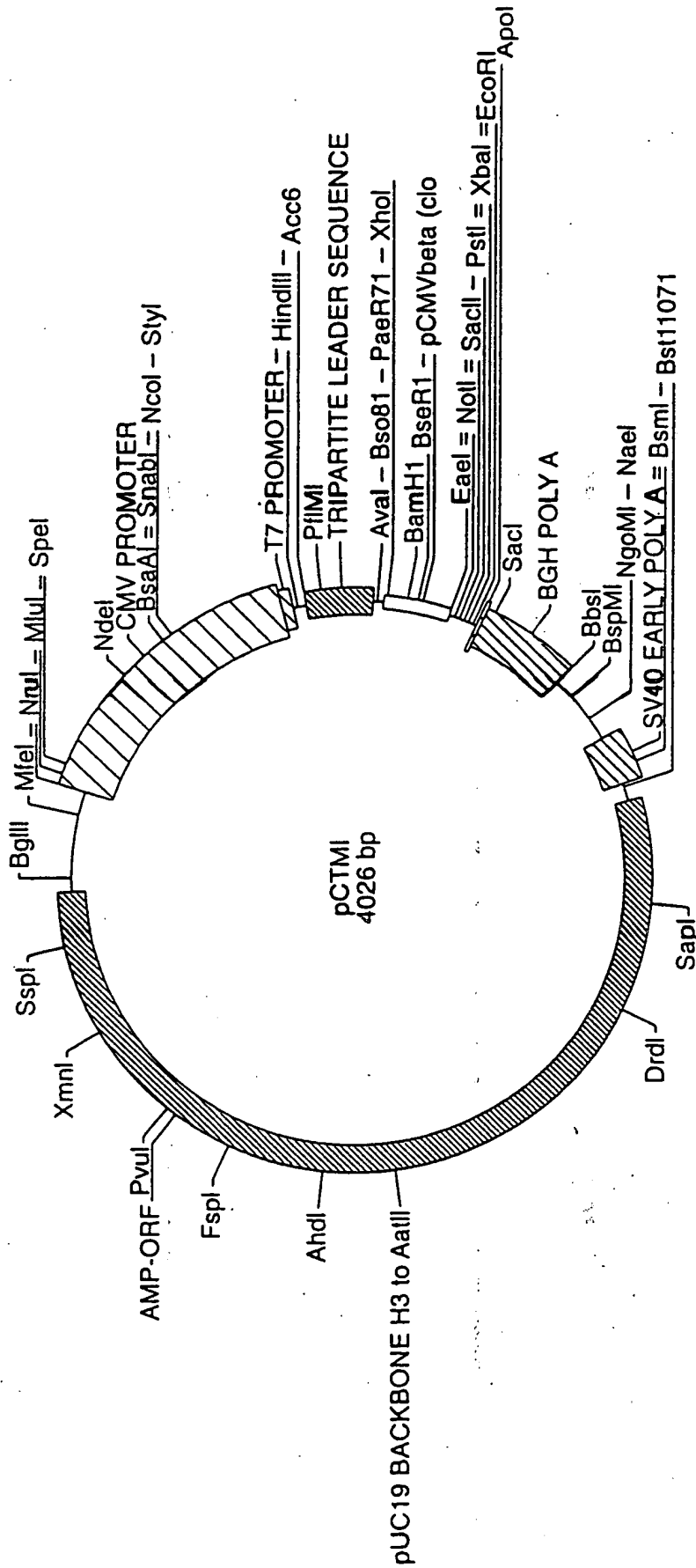


FIG. 5.



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```
>HincII
|
>AccI
||
>SalI
|||
>BglII
|
10 | 20 | 30 | 40 | 50 | 60
* | * | * | * | * | *
GACGGATCGG GAGATCTCCC GATCCCCCTAT GGTGCACTCT CAGTACAATC TGCTCTGATG

>AlwNI
|
70 | 80 | 90 | 100 | 110 | 120
* | * | * | * | * | *
CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT GGAGTGCCT GAGTAGTGCG

>ApoI
|
130 | 140 | 150 | 160 | 170 | 180
* | * | * | * | * | *
CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA CAATTGCATG AAGAATCTGC

>MfeI
|
190 | 200 | 210 | 220 | 230
* | * | * | * | *
TTAGGGTTAG GCGTTTTCGG CTGCTTCG CGA TGT ACG GGC CAG ATA TAC GCG TTG
Arg Cys Thr Gly Gln Ile Tyr Ala Leu
e e CMV PROMOTER e e

>NruI
|
190 | 200 | 210 | 220 | 230
* | * | * | * | *
TTAGGGTTAG GCGTTTTCGG CTGCTTCG CGA TGT ACG GGC CAG ATA TAC GCG TTG
Arg Cys Thr Gly Gln Ile Tyr Ala Leu
e e CMV PROMOTER e e

>AflIII
|
>MluI
|
>HincII
|
```

FIG. 6-1.

**FIG. 6-2.**



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+

```
>AatII
|
430 *
| *
TCA ATG GGT GGA CTA TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA
Ser Met Gly Gly Leu Phe Thr Val Asn Cys Pro Leu Gly Ser Thr Ser>
e e e e e CMV PROMOTER e e e e e >

>BglI
|
440 *
| *
450 *
460 *
470 *
TCA ATG GGT GGA CTA TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA
Ser Met Gly Gly Leu Phe Thr Val Asn Cys Pro Leu Gly Ser Thr Ser>
e e e e e CMV PROMOTER e e e e e >

>NdeI
|
480 *
| *
490 *
500 *
510 *
520 *
AGT GTA TCA TAT GCC AAG TAC GCC CCC TAT TGA CGT CAA TGA CGG TAA
Ser Val Ser Tyr Ala Lys Tyr Ala Pro Tyr *** Arg Gln *** Arg ***>
e e e e e CMV PROMOTER e e e e e >

>BglI
|
530 *
| *
540 *
550 *
560 *
570 *
ATG GCC CGC CTG GCA TTA TGC CCA GTA CAT GAC CTT ATG GGA CTT TCC
Met Ala Arg Leu Ala Leu Cys Pro Val His Asp Leu Met Gly Leu Ser>
e e e e e CMV PROMOTER e e e e e >

>BsaAI
|
580 *
| *
590 *
600 *
610 *
TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT
Tyr Leu Ala Val His Leu Arg Ile Ser His Arg Tyr Tyr His Gly Asp>
e e e e e CMV PROMOTER e e e e e >

>NcoI
|
>StyI >MslI
|
610 *
| *
TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT
Tyr Leu Ala Val His Leu Arg Ile Ser His Arg Tyr Tyr His Gly Asp>
e e e e e CMV PROMOTER e e e e e >
```

FIG 6-3.

**FIG. 6-4.**







+

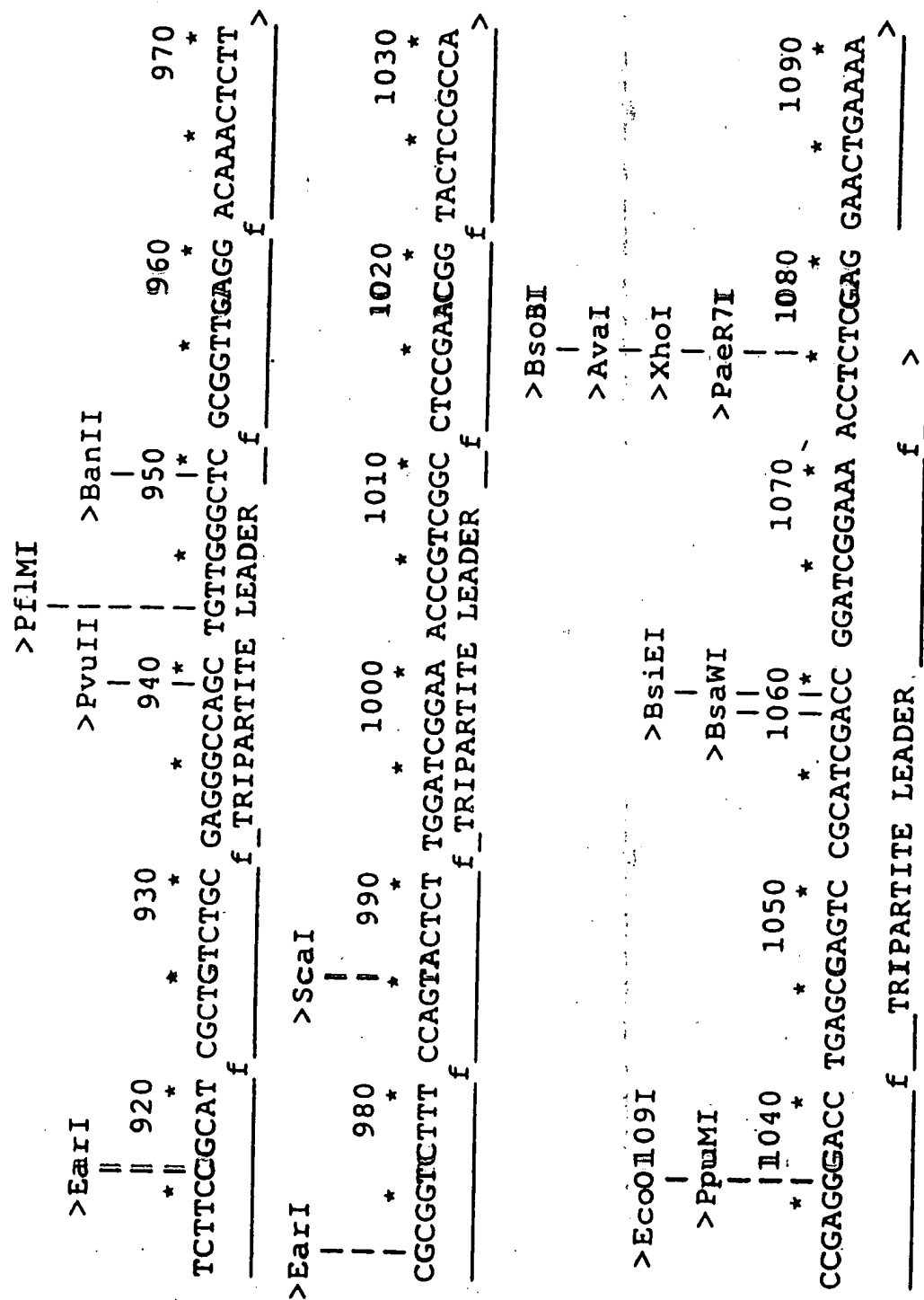


FIG. 6-6.



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+

```
>HincII          >EcoOI09I  >BsaWI
|                |         |
>HpaI           >PpuMI   >BamHI
|               |         |
1100 | 1110      1120      1130      1140      1150
*   *   *   *   *   *   *   *   *   *
ACGAGAAAGT TAACTGGTAA GTTAGTCTT TTTGTCTTT TATTCAGGT CCCGGATCCG
b_ HYBRID SV40 LATE INTRON b_ >

>BseRI          >StuI
|                |
1160 | 1170      1180      1190      1200      1210
*   *   *   *   *   *   *   *
GTGGTGGTGC AAATCAAGA ACTGCTCCTC AGTGGATGTT GCCTTACTT CTAGGCCTGT
b_ HYBRID SV40 LATE INTRON b_ >

>BsiEI          >EagI    >XbaI
|                |         |
>EaeI          >SacII   >PstI
|               |         |
>NotI          >SfcI    |
|               |         |
1220 | 1230      1240      1250      1260      1270
*   *   *   *   *   *   *   *
ACGGAAGTGT TACTTCTGCT CTAAAGCTG CGGAATTGTA CCCGGGGCCG CTGCAGTCTA
b_ HYBRID SV40 LATE INTRON b_ >
```

FIG. 6-7.



+

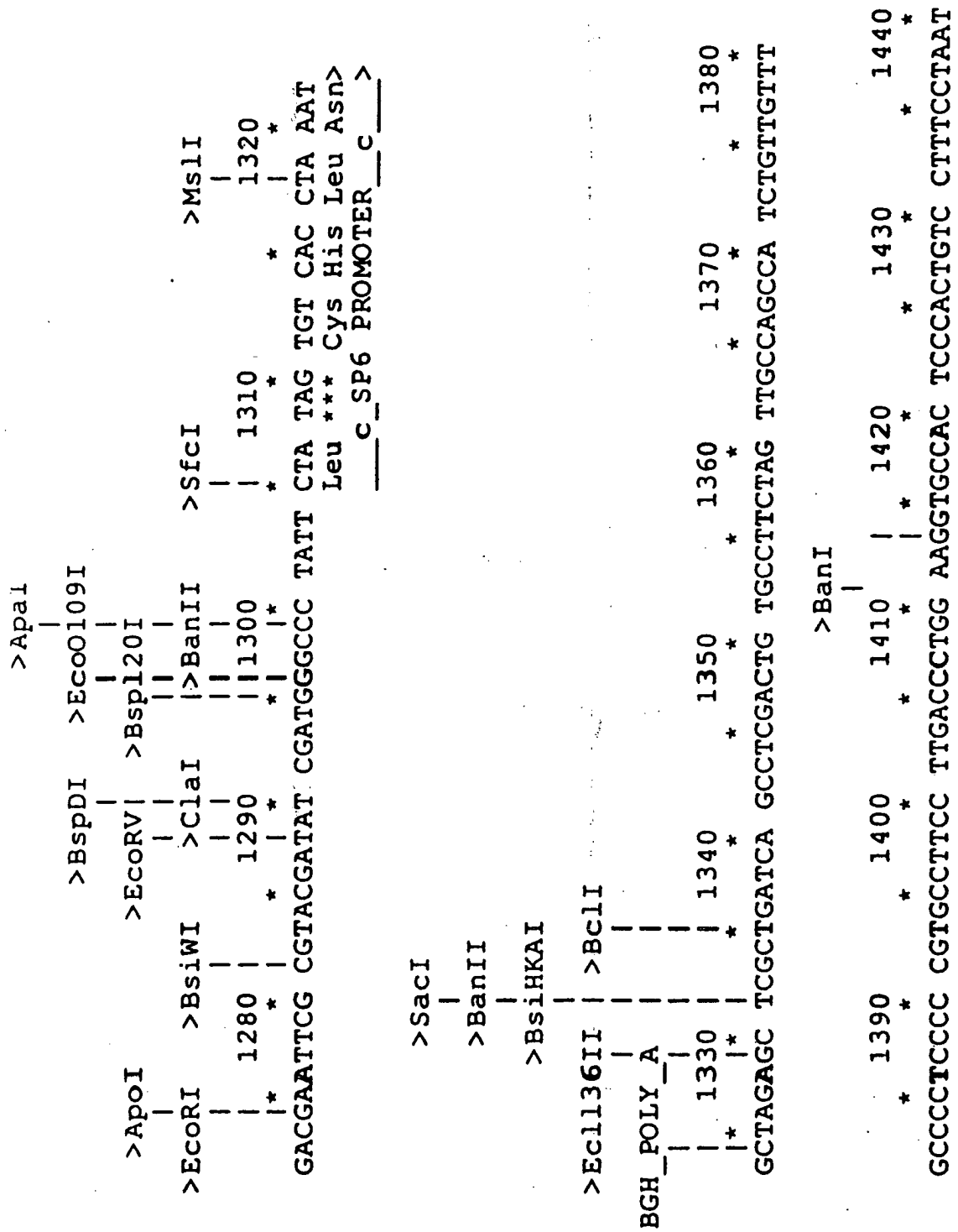


FIG. 6-8.



```

1450 * 1460 1470 1480 1490 1500
* * * * *
AAAATGAGGA AATTGCATCG CATTGTCTGA GTAGGTGTCA TTCTATTCTG GGGGTGGGG
>BbsI
1510 1520 1530 1540 1550 1560
* * * * *
TGGGGCAGGA CAGCAAGGGG GAGGATTGGG AAGACAATAG CCGAAATGAC CGACCAAGCG
>BspMI
>BssSI
1570 1580 1590 1600 1610 1620
* * * * *
ACGCCCAACC TGCCATCACC AGATTTCGAT TCCACCGCCG CCTTCTATGA AAGGTTGGCG
>NaeI
>NgoMI
>BpmI
>BsrFI
1630 1640 1650 1660 1670 1680
* * * * *
TTCGGAATCG TTTTCCGGGA CGCCGGCTGG ATGATCCTCC AGCGCCGGGA TCTCATGCTG

```

FIG 6-9.

+



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```
>BpmI
|
>SV40_early_poly_A
|
1690 * 1700 1710 1720 1730 1740
* * |* * * * *
GAGTTCTTCG CCCACCCCAA CTTGTTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT

>ApoI
|
1750 * 1760 1770 1780 1790 1800
* * * * *
AGCATCACAA ATTCACAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TGGTTTGTC

>BsmI
|
1750 * 1760 1770 1780 1790 1800
* * * * *
AGCATCACAA ATTCACAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TGGTTTGTC

>HincII
|
>Bst1107I >AccI
| |
>AccI >Sali
| | | |
1810 * 1820 1830 1840 1850 1860
* * * * *
AAACTCATCA ATGTATCTTA TCATGTCTGT ATACCGTCGA CCTCTAGCTA GAGCTTGGCG

>BsrBI
|
1870 * 1880 1890 1900 1910 1920
* * * * *
TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC CGCTCACAAT TCCACACAAC
d d PUC19 BACKBONE d d
```

FIG. 6-10.



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+

>BamI  
1930 \* 1940 \* 1950 \* 1960 \* 1970 \* 1980 \*  
ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT AATGAGTGAG CTAACATCACA  
d d PUC19 BACKBONE d d  
>

>AseI  
1990 \* 2000 \* 2010 \* 2020 \* 2030 \* 2040 \*  
TTAATTGCGT TGGGCTCACT GCCCGCTTC CAGTCGGGAA ACCTGTCGTG CCAGCTGCAT  
d d PUC19 BACKBONE d d  
>

>EaeI  
2050 \* 2060 \* 2070 \* 2080 \* 2090 \* 2100 \*  
TAATGAATCG GCCAAGCGC GGGAGAGGC GGTTGCGTA TTGGGGCGCTC TTCCGCTTCC  
d d PUC19 BACKBONE d d  
>

FIG. 6-11.



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+

```
>BsiEI
2110 * 2120 * 2130 * 2140 * 2150 * 2160 *
TCGCTCACTG ACTCGCTGGC CTCGGTCGTT CGGCTGCGGC GAGCGGTATC AGCTCACTCA
d d PUC19 BACKBONE d d d d d d >

>AflIII
2170 * 2180 * 2190 * 2200 * 2210 * 2220 *
AAGCGGTAA TACGGTTATC CACAGAATCA GGGGATAACG CAGGAAAGAA CATGTGAGCA
d d d PUC19 BACKBONE d d d d d d >

2230 * 2240 * 2250 * 2260 * 2270 * 2280 *
AAAGGCCAGC AAAAGGCCAG GAACCGTAAA AAGCCGCGGT TGCTGGCGTT TTTCCATAGG
d d d PUC19 BACKBONE d d d d d d >

>DrdI
2290 * 2300 * 2310 * 2320 * 2330 * 2340 *
CTCCGCCCC CTGACGAGCA TCACAAAAT CGACGCTCAA GTCAGAGGTG GCGAAACCCG
d d d PUC19 BACKBONE d d d d d d >

>BssSI
2350 * 2360 * 2370 * 2380 * 2390 * 2400 *
ACAGGACTAT AAAGATACCA GCGTTTCCC CCTGGAAGCT CCCTCGTGCG CTCTCCTGTT
d d d PUC19 BACKBONE d d d d d d >
```

FIG 6-12.



**FIG. 6-13.**



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+

>Sfci									
2650	*	2660	*	12670	*	2680	*	2690	2700
AGCAGAGCGA GGTATGTAGG CCGTGCTACA GAGTTCTTGA AGTGGTGGCC TAACTACGGC									
d d PUC19 BACKBONE d d									
>									
>Eco57I									
2710	*	2720	*	2730	*	2740	*	2750	2760
TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGCTGA AGCCAGTTAC CTTCGGGAAA									
d d PUC19 BACKBONE d d									
>									
2770	*	2780	*	2790	*	2800	*	2810	2820
AGAGTTGGTA GCTCTTGATC CGGCAACAAC ACCACCGCTG GTAGCGGTGG TTTTITTTGTT									
d d PUC19 BACKBONE d d									
>									
2830	*	2840	*	2850	*	2860	*	2870	2880
TGCAAGCAGC AGATTACGG CAGAAAAAA GGATCTCAAG AAGATCCTTT GATCTTTTCT									
d d PUC19 BACKBONE d d									
>									
>BspHI									
2890	*	2900	*	2910	*	2920	*	2930	2940
ACGGGGTCTG ACGCTCAGTG GAACGAAAC TCACGTTAAG GGATTTTGGT CATGAGATTA									
d d PUC19 BACKBONE d d									
>									

FIG 6-14.



+

>DraI  
|  
2950 \* 2960 \* 2970 \* 2980 \* 2990 \* 3000 \*  
TCAAAAAGGA TCCTCACCTA GATCCTTTTA AATTAAAAAT GAAGTTTAA ATCAATCTAA  
d d PUC19 BACKBONE d d

>BanI  
|  
3010 \* 3020 \* 3030 \* 3040 \* 3050 \* 3060 \*  
AGTATATG AGTAAACTTG GTCTGACAGT TACCAATGCT TAATCAGTGA GGCACCTATC  
a AMP-ORF a  
d d PUC19 BACKBONE d d

>AhdI  
|  
3070 \* 3080 \* 3090 \* 3100 \* 3110 \* 3120 \*  
TCAGCGATCT GTCTATTTCG TTCATCCATA GTTGCCTGAC TCCCCGTCGT GTAGATAACT  
a AMP-ORF a  
d d PUC19 BACKBONE d d

>BsaI  
|  
>BsrDI >BpmI  
|  
3130 \* 3140 \* 3150 \* 3160 \* 3170 \* 3180 \*  
ACGATACGGG AGGGCTTACC ATCTGGCCCC AGTGCCTGCAA TGATACCGCG AGACCCACGC  
a AMP-ORF a  
d d PUC19 BACKBONE d d

FIG. 6-15.



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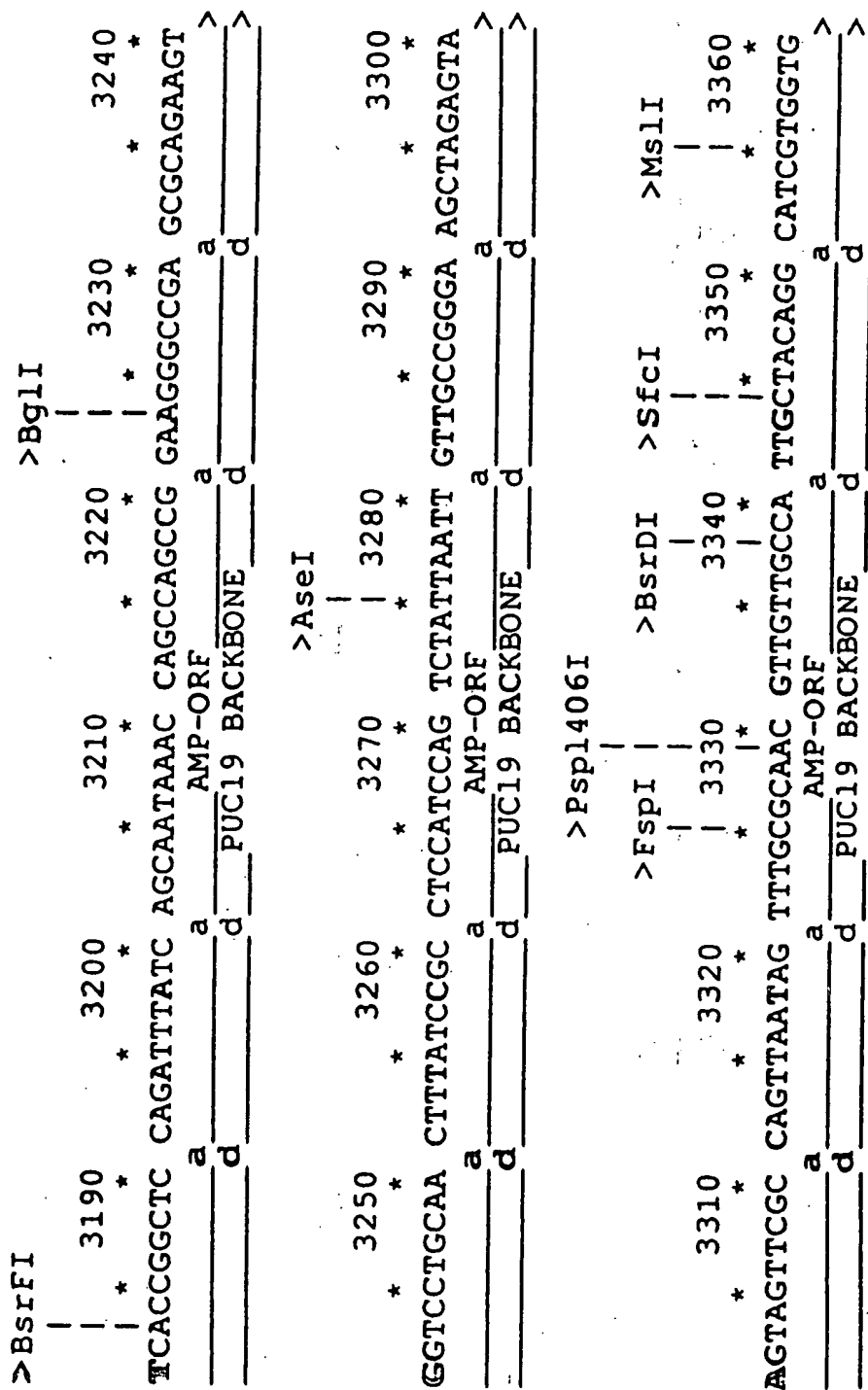


FIG 6-16.



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>BsaWI  
3370 3380 3390 3400 3410 3420  
\* \* \* \* \*  
TCACGCTCGT CGTTGGTAT GGCTTCATC AGCTCCGGT CCAACGATC AAGCGAGTT  
a a AMP-ORF a  
d d PUC19 BACKBONE d d

>BsiEI  
3430 3440 3450 3460 3470 3480  
\* \* \* \* \*  
ACATGATCCC CCATGTTGTG CAAAAAGCG GTTAGCTCCT TCGGTCCTCC GATCGTTGTC  
a a AMP-ORF a  
d d PUC19 BACKBONE d d

>EaeI  
3490 3500 3510 3520 3530 3540  
\* \* \* \* \*  
AGAAGTAAGT TGGCCGCAGT GTTATCACTC ATGGTTATGG CAGCACTGCA TAATTCTCTT  
a a AMP-ORF a  
d d PUC19 BACKBONE d d

>MslI  
3490 3500 3510 3520 3530 3540  
\* \* \* \* \*  
AGAAGTAAGT TGGCCGCAGT GTTATCACTC ATGGTTATGG CAGCACTGCA TAATTCTCTT  
a a AMP-ORF a  
d d PUC19 BACKBONE d d

>ScaI  
3500 3560 3570 3580 3590 3600  
\* \* \* \* \*  
ACTGTCATGC CATCCGTAAG ATGCTTTTCT GTGACTGGTG AGTACTCAAC CAAGTCATTC  
a a AMP-ORF a  
d d PUC19 BACKBONE d d

FIG. 6-17.



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+

```
>BsiEI
3610      *      3620      *      3630      *      3640      *      3650      *      3660      *
TGAGAAATAGT GTATGCGGGG ACCGAGTTC TCTTGCCCGG CGTCAATACG GGATAATACC
a      d      a      d      AMP-ORF      a      d      a      d      >
PUC19 BACKBONE      d      >

>PspI406I
3670      *      3680      *      3690      *      3700      *      3710      *      3720      *
GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTTGAA AACGTTCTTC GGGGCGAAAA
a      d      a      d      AMP-ORF      a      d      a      d      >
PUC19 BACKBONE      d      >

>ApaLI
3730      *      3740      *      3750      *      3760      *      3770      *      3780      *
CTCTCAAGGA TCTTACCGCT GTTGAGATCC AGTTCGATGT AACCCACTCG TGCACCCAAC
a      d      a      d      AMP-ORF      a      d      a      d      >
PUC19 BACKBONE      d      >

>BssSI | >BsiHKAI
3770      *      3780      *
TGCACCCAAC
a      d      a      d      >
PUC19 BACKBONE      d      >

>Eco57I
```

FIG. 6-18.





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```

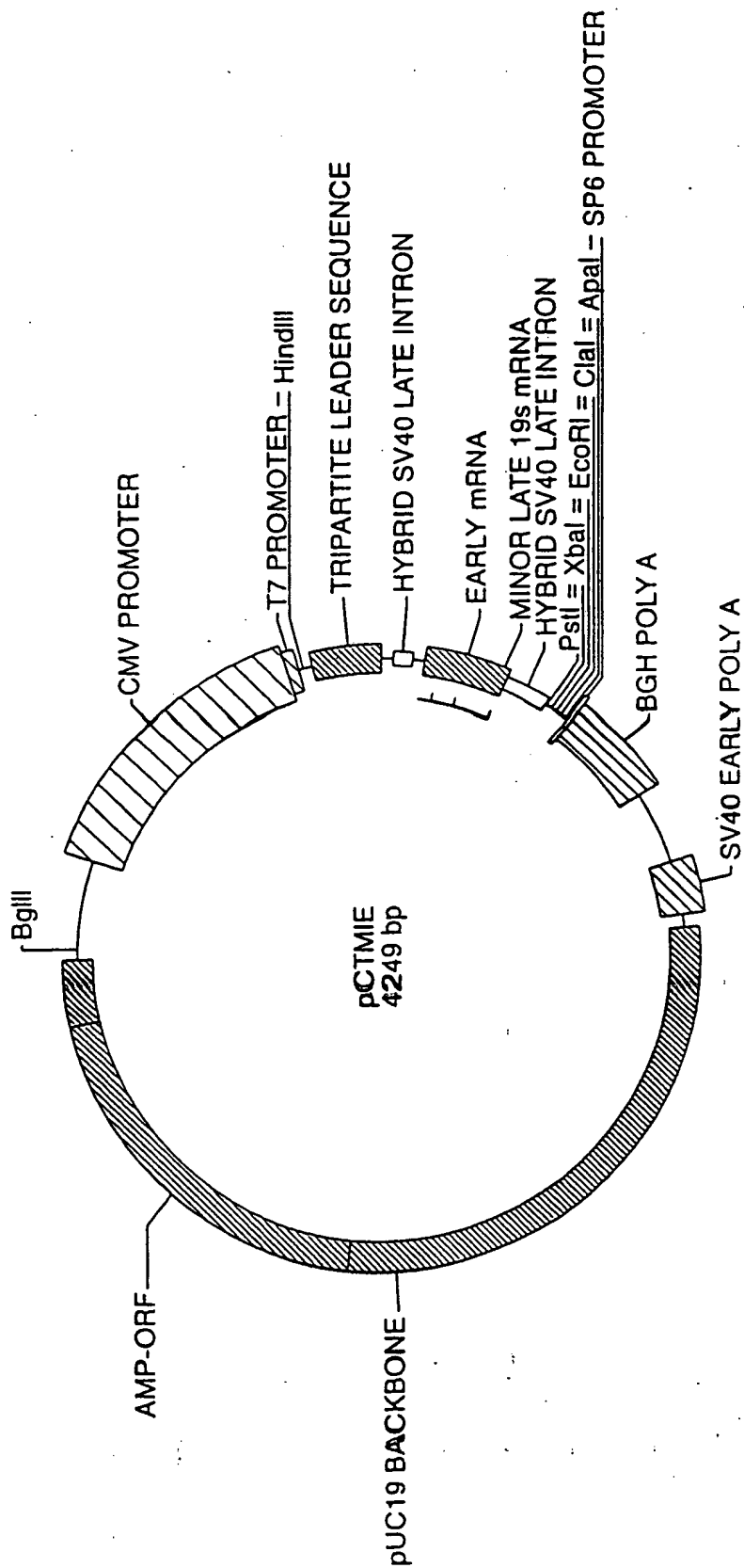
3970      * 3980      * 3990      * 4000      * 4010      * 4020      *
TGTATTGAGA AAAATAAACA AATAGGGGTT CCGCGCACAT TTCCCCGAAA AGTGCCACCT
      d      d      d      d      d      d      d      d
>HincII
      |
>AatII
      ||
>AccI
      ||
>SalI
      |||
      |*|
GACGTC
      >

```

FIG. 6-20.

|||||





**FIG. 7.**

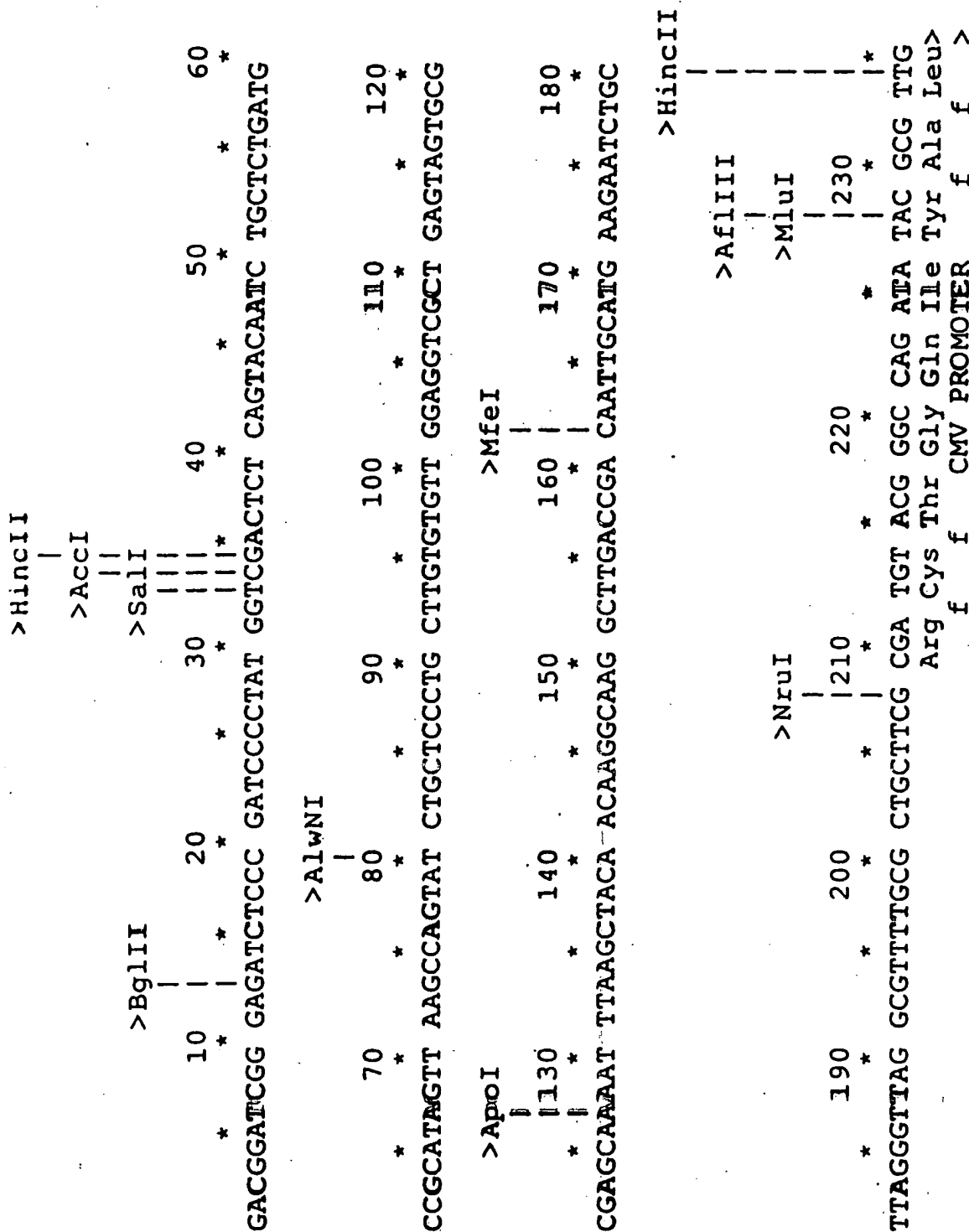


FIG. 8-1.

**FIG. 8-2.**



**FIG 8-4.**



```

>PflMI
|
>EarI          >PvuII          >BamII
|              |              |
* | 920        * | 940        * | 950        * | 960        * | 970
* | *          * | *          * | *          * | *          * | *
TCTTCCGCAT CGCTGTCTGC GAGGCCAGC TGTGGGCTC GCGTTGAGG ACAAACTCTT
g          g          g          g          g          g          g
TRIPARTITE LEADER SEQUENCE

>EarI          >ScaI
|              |
* | 980        * | 990        * | 1000       * | 1010       * | 1020       * | 1030
* | *          * | *          * | *          * | *          * | *          * | *
CGCGGTCTTT CCAGTACTCT TGGATCGGAA ACCCGTCGGC CTCCGAACGG TACTCCGCCA
g          g          g          g          g          g          g
TRIPARTITE LEADER SEQUENCE

>XhoI
|
>AvaI
|
>BsoBI
|
>PaeR7I
|
>EcoO109I      >BsiEI
|              |
>PpuMI          >BsaWI
|              |
* | 1040        * | 1050        * | 1060        * | 1070        * | 1080        * | 1090
* | *          * | *          * | *          * | *          * | *          * | *
CCGAGGGACC TGAGCGAGTC CGCATCGACC GGATCGGAAA ACCTCTCGAG GAACTGAAAA

```

FIG 8-6.

+



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TRIPARTITE LEADER SEQUENCE \_\_\_\_\_>  
g \_\_\_\_\_>  
\_\_\_\_\_  
>HpaI  
|  
>HincII  
|  
1100 | 1110 | 1120 | 1130 | 1140 | 1150  
\* | \* | \* | \* | \* | \*  
ACCAGAAAGT TAACTGGTAA GTTAGTCTT TTGTCTTT TATTCAGGT CCCGGATCTG  
b \_\_\_\_\_ HYBRID SV40 LATE INTRON b \_\_\_\_\_>

>PpuMI  
|  
>EcoOI09I  
|  
1160 | 1170 | 1180 | 1190 | 1200 | 1210  
\* | \* | \* | \* | \* | \*  
AGTTAGGGCG GGACATGGGC GGAGTTAGGG GCGGGACTAT GGTGCTGAC TAATTGAGAT  
< \_\_\_\_\_ h \_\_\_\_\_ h \_\_\_\_\_>  
h EARLY MRNA

>SphI  
|  
>NsiI  
|  
1220 | 1230 | 1240 | 1250 | 1260 | 1270  
\* | \* | \* | \* | \* | \*  
GCATGCTTGG CATACTTCTG CCTGCTGGGG AGCCTGGGGA CTTCCACAC CTGGTTGCTG  
< \_\_\_\_\_ h \_\_\_\_\_ h \_\_\_\_\_>  
h EARLY MRNA

<72\_bp\_tandem\_repeat\_enhancer\_sequence\_

FIG. 8-7.



**FIG. 8-8.**





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+

1570 \* 1580 \* 1590 \* 1600 \* 1610 \* 1620 \*  
TCAGCCTCGA CTGTGCCTTC TAGTTGCCAG CCATCTGTTG TTGCCCCCTC CCCCCTGCCT

>Bani

1630 \* 1640 \* 1650 \* 1660 \* 1670 \* 1680 \*  
TCCTTGACCC TGGAGGGTGC CACTCCCCT GTCCCTTTCCT AATAAAATGA GGAATTCGA

1690 \* 1700 \* 1710 \* 1720 \* 1730 \* 1740 \*  
TCGCATTGTC TGAGTAGGTG TCATTCTATT CTGGGGGGTG GGGTGGGGCA GGACAGCAAG

>BspMI

>BbsI

1750 \* 1760 \* 1770 \* 1780 \* 1790 \* 1800 \*  
GGGGAGGATT GGGAAGACAA TAGCCGAAT GACCGACCAA GCGACGCCCA ACCTGCCATC

1810 \* 1820 \* 1830 \* 1840 \* 1850 \* 1860 \*  
ACGAGATTTC GATTCCACCG CCGCCTTCTA TGAAGGTG GGCTTCGGAA TCGTTTCCG

FIG 8-10.

**FIG. 8-11.**



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+

```
>HincII
|
>Bst1107I >AccI
| |
>AccI >SalI
| | |
2050 * * * 2060 * * * 2070 * * * 2080 * * * 2090 * * * 2100 * * *
TTATCATGTC TGTATACCGT CGACCTCTAG CTAGAGCTTG GCGTAATCAT GGTCATAGCT
PUC19 BACKBONE >

>BsrBI
|
2110 * * * 2120 * * * 2130 * * * 2140 * * * 2150 * * * 2160 * * *
GTTTCCTGTG TGAATTGTT ATCCGCTCAC AATCCACAC AACATACGAG CCGGAAGCAT
e e PUC19 BACKBONE e e

>BamI
|
2170 * * * 2180 * * * 2190 * * * 2200 * * * 2210 * * * 2220 * * *
AAAGTGTAAG GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATG CGTTGGCGTC
e e PUC19 BACKBONE e e

>PvuII >AseI >EaeI
| | |
2230 * * * 2240 * * * 2250 * * * 2260 * * * 2270 * * * 2280 * * *
ACTGCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAAATGAA TCGGCCAACG
e e PUC19 BACKBONE e e
```

FIG 8-12.



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```
>SapI
|
>HaeII      >EaRI
|           |
2290      2300      2310      2320      2330      2340
*          *          *          *          *          *
CGCGGGGAGA GCGGTTTGC GTATTGGCG CTCTCCGCT TCCTCGCTCA CTGACTCGCT
e          e          PUC19 BACKBONE e          e          >

>BsiEI      >BsrBI
|           |
2350      2360      2370      2380      2390      2400
*          *          *          *          *          *
GCGCTCGGTC GTTCGGCTGC GCGAGCGGT ATCAGCTCAC TCAAAGGCGG TAATACGGTT
e          e          PUC19 BACKBONE e          e          >

>AflIII
|
2410      2420      2430      2440      2450      2460
*          *          *          *          *          *
ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAGGCC AGCAAAGGC
e          e          PUC19 BACKBONE e          e          >

2470      2480      2490      2500      2510      2520
*          *          *          *          *          *
CAGGAACCGT AAAAAGCCCG CGTTGCTGGC GTTTTCCAT AGGCTCCGCC CCCCTGACGA
e          e          PUC19 BACKBONE e          e          >
```

FIG. 8-13.

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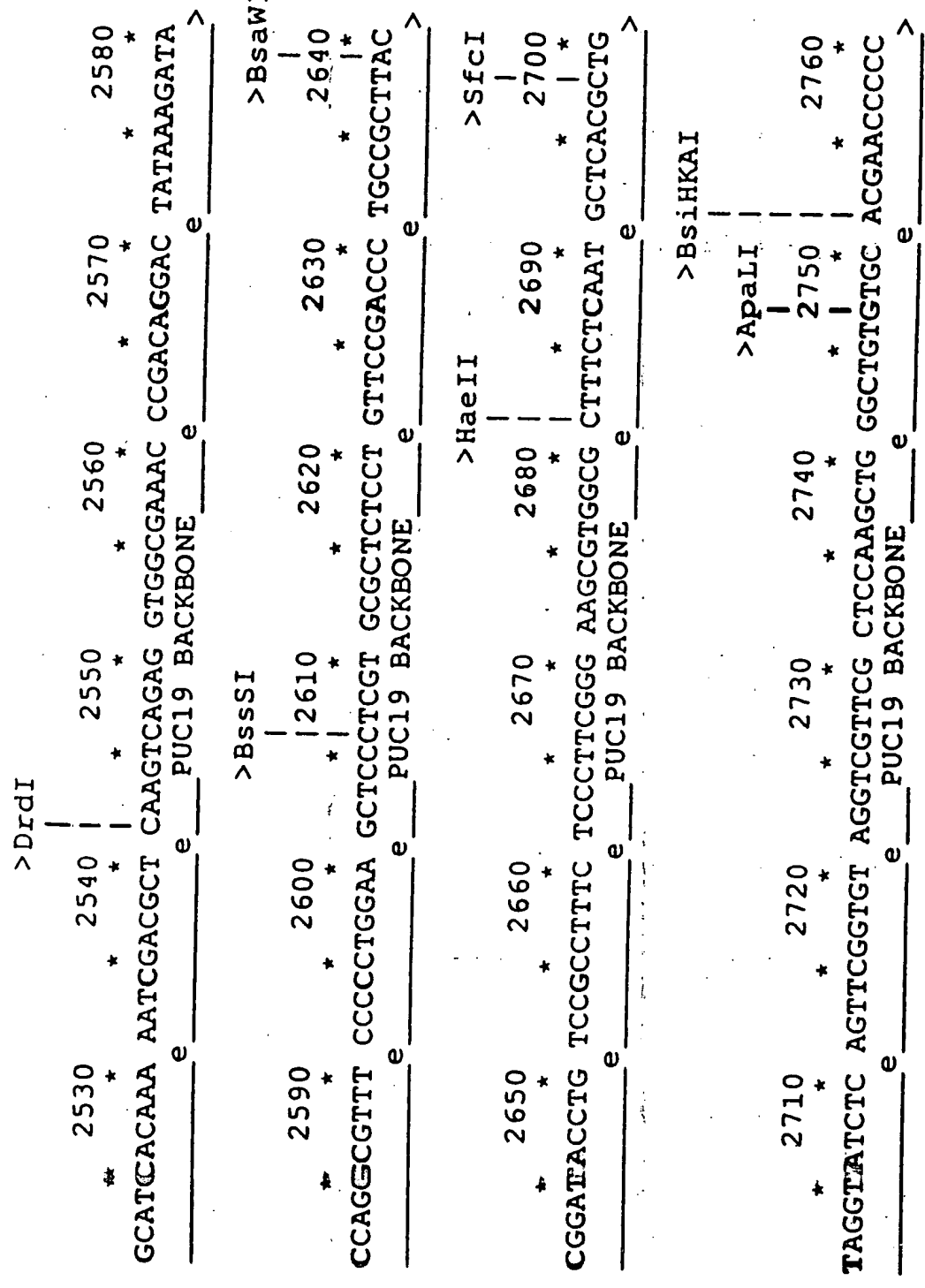


FIG. 8-14.



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```
>BsiEI          >BsaWI
2770  *  | 2780  *  | 2790  *  | 2800  *  | 2810  *  | 2820  *
CGTTCAGCCC GACCGCTGCG CCTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG
e          e          e          e          e          e
PUC19 BACKBONE

>AlwNI
2830  *  | 2840  *  | 2850  *  | 2860  *  | 2870  *  | 2880  *
ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT
e          e          e          e          e          e
PUC19 BACKBONE

>SfcI
2890  *  | 2900  *  | 2910  *  | 2920  *  | 2930  *  | 2940  *
AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT
e          e          e          e          e          e
PUC19 BACKBONE

>Eco57I
2950  *  | 2960  *  | 2970  *  | 2980  *  | 2990  *  | 3000  *
ATTTGGTATC TCGGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTGT GTAGCTCTTG
e          e          e          e          e          e
PUC19 BACKBONE
```

FIG 8-15.



3010	*	3020	*	3030	*	3040	*	3050	*	3060	*
ATCCGGGCAA	e	CAAACCA	CG	CTGGTAGCGG	TGGTTTTTTT	GTTTGCAAGC	AGCAGATTAC				
				PUC19	BACKBONE	e					
3070	*	3080	*	3090	*	3100	*	3110	*	3120	*
GCGCAGAAAA	e	AAAGGATCTC	AAGAAGATCC	TTTGATCTTT	TCTACGGGGT	CTGACGGCTCA					
				PUC19	BACKBONE	e					
>BspHI											
3130	*	3140	*	3150	*	3160	*	3170	*	3180	*
GTGGAACGAA	e	AATCAGCTT	AAGGGATTT	GGTCATGAGA	TTATCAAAAA	GGATCTTCAC					
				PUC19	BACKBONE	e					
>DraI											
3190	*	3200	*	3210	*	3220	*	3230	*	3240	*
CTAGATCCCT	e	TTAAATTAA	AATGAAGTTT	TAAATCAATC	TAAAGTATAT	ATGAGTAAAC					
				PUC19	BACKBONE	e					
>BspHI											
3250	*	3260	*	3270	*	3280	*	3290	*	3300	*
TTGGTCTGAC	e	AGTTACCAAT	GCTTAATCAG	TGAGGCACCT	ATCTCAGCGA	TCTGTCTATT					
				a	AMP-ORF	a					
				PUC19	BACKBONE	e					

FIG. 8-16.



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>AhdI  
|  
3310 \* 3320 \* 3330 \* 3340 \* 3350 \* 3360 \*  
TCGTTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT  
a e a AMP-ORF a a  
e e PUC19 BACKBONE e e

>BsaI  
|  
>BsrDI >BpmI >BsrFI  
| | |  
3370 \* 3380 \* 3390 \* 3400 \* 3410 \* 3420 \*  
ACCATCTGGC CCCAGTGCTG CAATGATACC GCGAGACCCA CGCTCACC GG CTCCAGATTT  
a e a AMP-ORF a a  
e e PUC19 BACKBONE e e

>BglI  
|  
3430 \* 3440 \* 3450 \* 3460 \* 3470 \* 3480 \*  
ATCAGCAATA AACGAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCTCG CAACCTTATC  
a e a AMP-ORF a a  
e e PUC19 BACKBONE e e

FIG. 8-17.



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>AseI  
3490 \* 3500 3510 3520 3530 3540  
\* \* \* \* \*  
CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA  
a a AMP-ORF a a  
e e PUC19 BACKBONE e e

>PspI406I  
>EspI | >BsrDI | >SfcI | >MslI  
3550 | 3560 | 3570 | 3580 | 3590 | 3600  
\* | \* | \* | \* | \* | \*  
TAGTTGCGC AACGTTGTTG CCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCGTTGG  
a a AMP-ORF a a  
e e PUC19 BACKBONE e e

>BsaWI  
3610 3620 3630 3640 3650 3660  
\* \* \* \* \*  
TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT  
a a AMP-ORF a a  
e e PUC19 BACKBONE e e

>BsiEI | >EaeI  
>PvuI |  
3670 3680 3690 3700 3710 3720  
\* \* \* \* \*  
GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC  
a a AMP-ORF a a  
e e PUC19 BACKBONE e e

FIG. 8-18.



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>MslI  
|  
3730 \* 3740 \*  
AGTGGTTATCA CTCATGGTTA TGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT  
a a AMP-ORF a  
e e PUC19 BACKBONE e e  
>>

>ScaI  
|  
3790 \* 3800 \* 3810 \* 3820 \* 3830 \* 3840 \*  
AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG  
a a AMP-ORF a  
e e PUC19 BACKBONE e e  
>>

>BsiEI  
|  
3850 \* 3860 \* 3870 \* 3880 \* 3890 \* 3900 \*  
GCGACCGAGT TGCTCTTGCC CGGCGTCAAT ACGGGATAAT ACCGGGCCAC ATAGCAGAAC  
a a AMP-ORF a  
e e PUC19 BACKBONE e e  
>>

>PspI406I  
|  
>DraI >BsiHKAI >XmnI  
| | |  
3910 \* 3920 \* 3930 \* 3940 \* 3950 \* 3960 \*  
TTTAAAGTG CTCATCATTTG GAAAACGTTT TTCGGGGCGA AAACCTCTCA GGATCTTACC  
a a AMP-ORF a  
e e PUC19 BACKBONE e e  
>>

FIG. 8-19.



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```
>Eco57I
|
>ApaLI
|
>BssSI |>BsiHKAI
|      |
3970   * 3980   * 3990   * 4000   * 4010   * 4020   *
GCTGTTGAGA TCCAGTTTGA TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT
a      a      a      a      a      a
e      e      e      e      e      e
PUC19 BACKBONE

4030   * 4040   * 4050   * 4060   * 4070   * 4080   *
TACTTTCACC AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAATGCCG CAAAAAAGGG
a      a      a      a      a      a
e      e      e      e      e      e
PUC19 BACKBONE

>MslI
||
4090   * 4100   * 4110   * 4120   * 4130   * 4140   *
AATAAGGGCG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTC AAT ATTATGAAG
a      a      a      a      a      a
e      e      e      e      e      e
PUC19 BACKBONE

>EarI >SspI
|      |
4120   * 4130   * 4140   *
```

FIG. 8-20.

**FIG. 8-21.**



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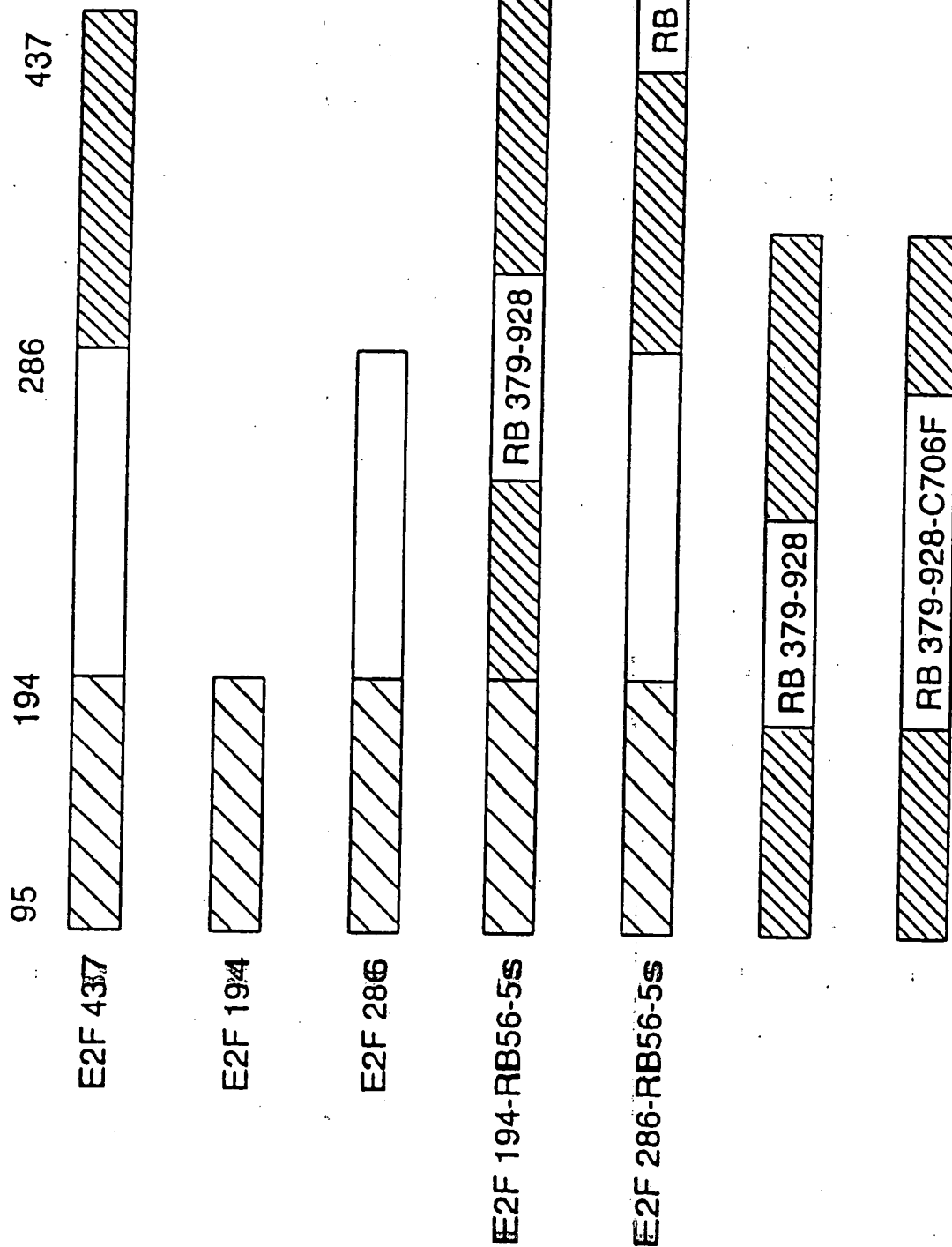


FIG. 9

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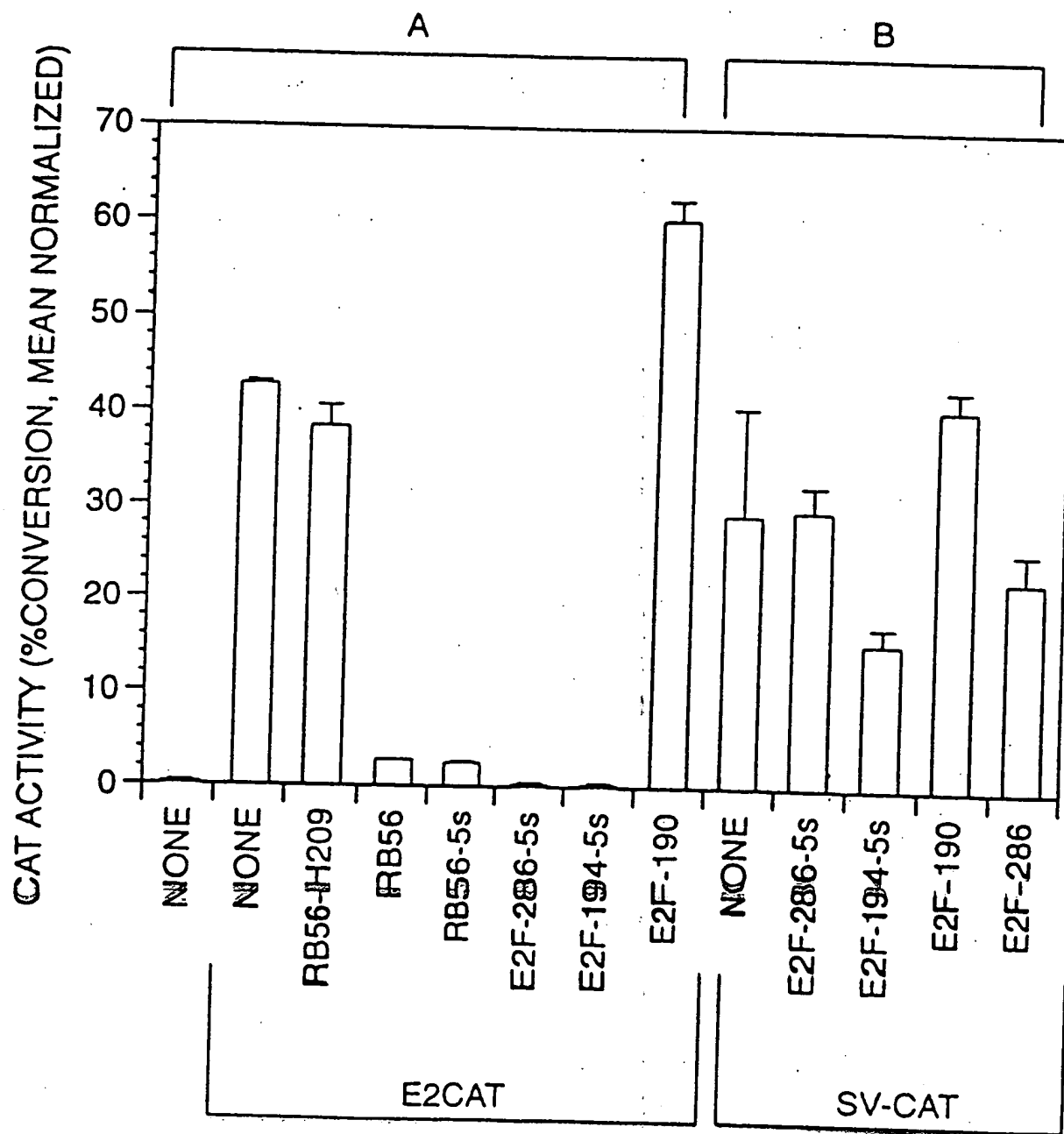


FIG. 10





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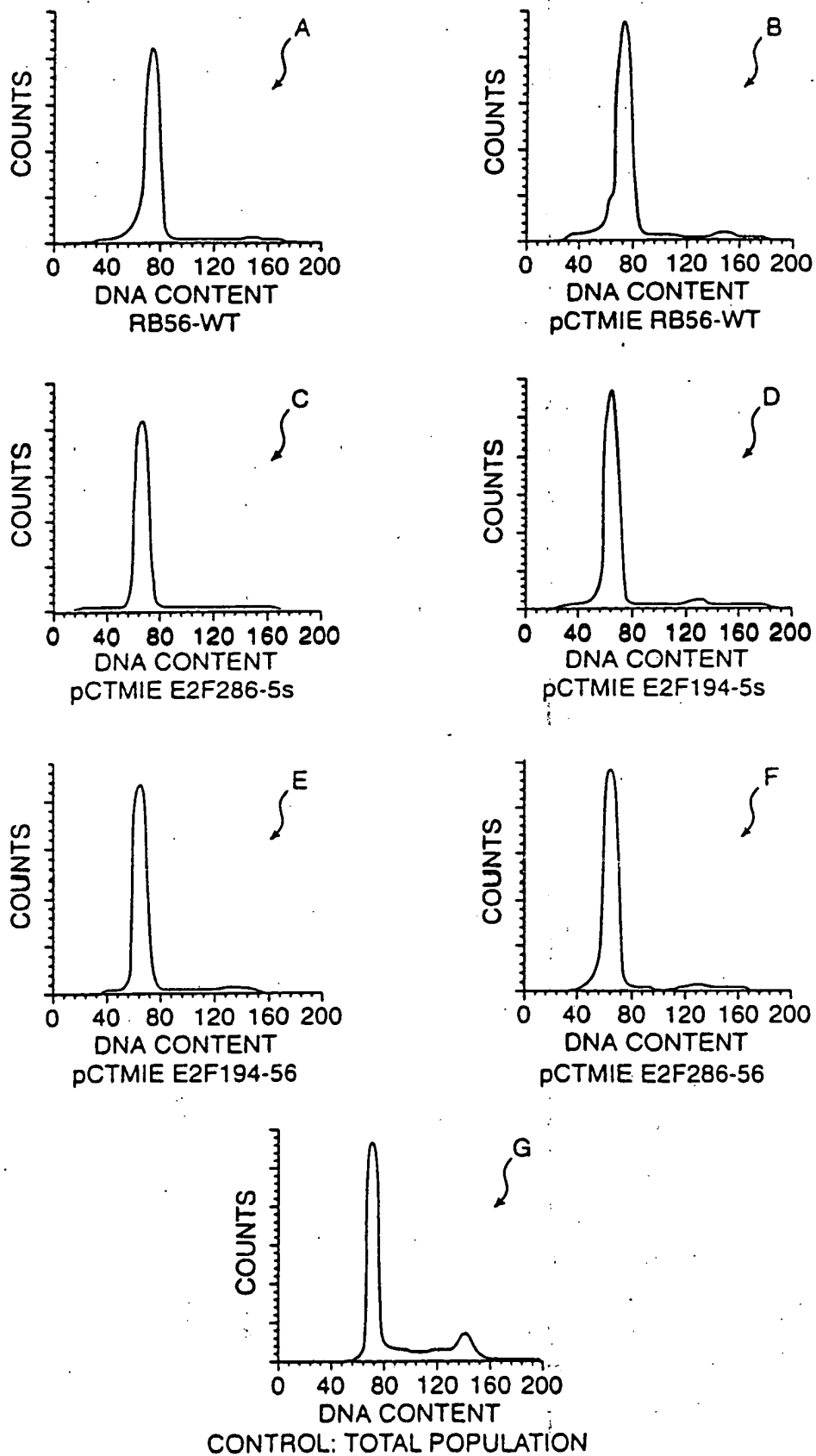


FIG. 12



+

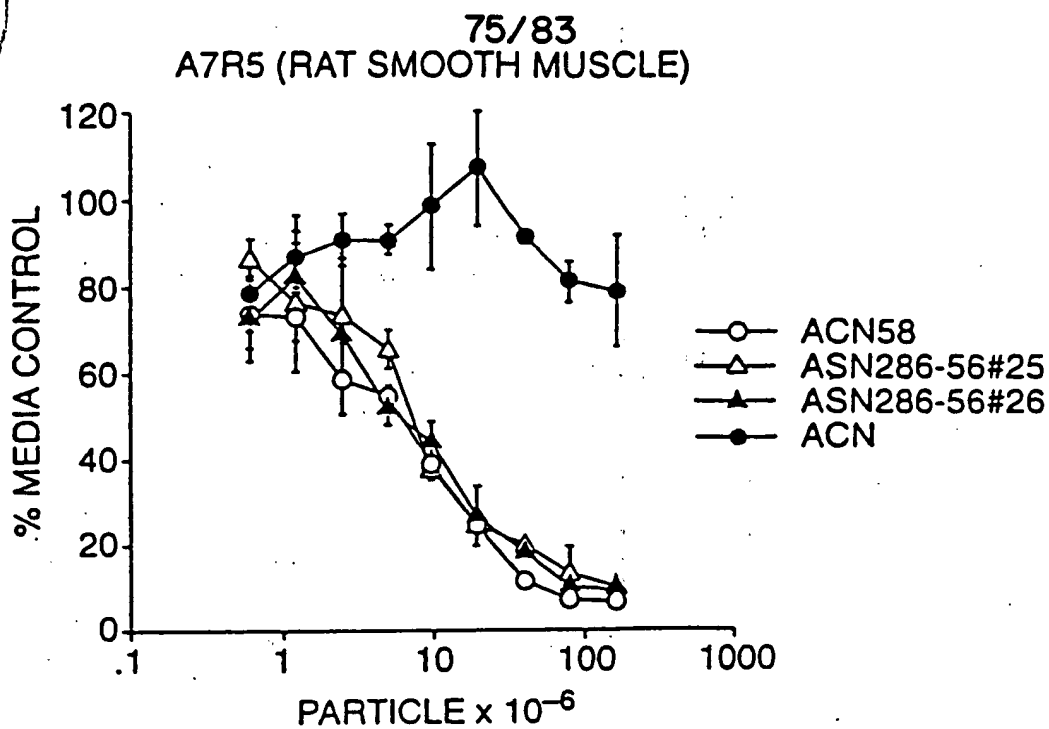


FIG. 13A

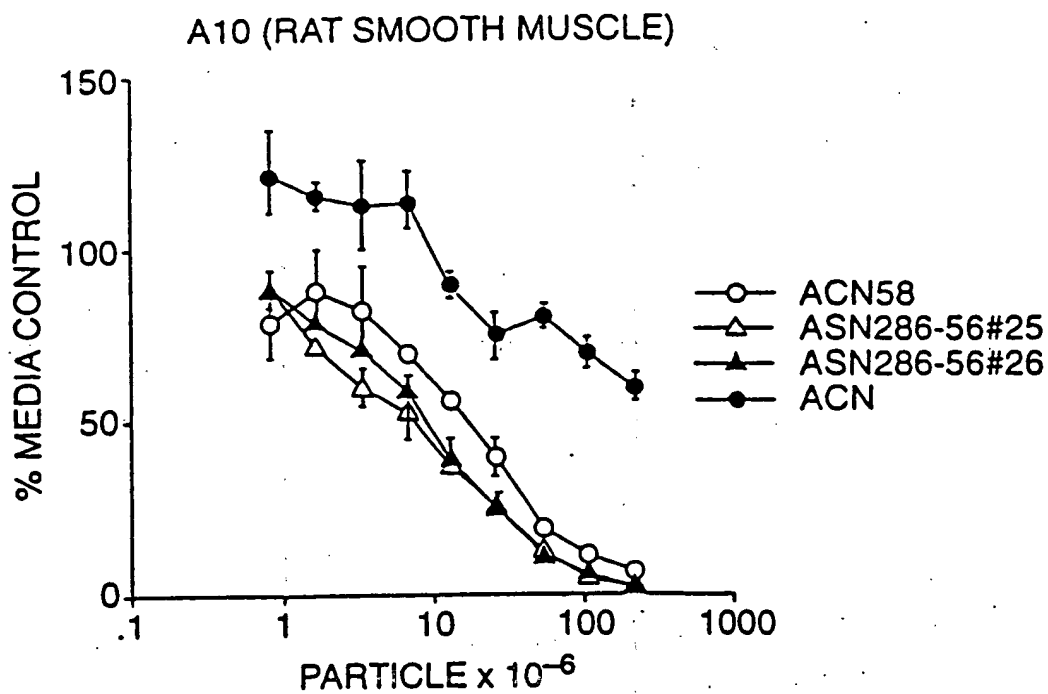


FIG. 13B



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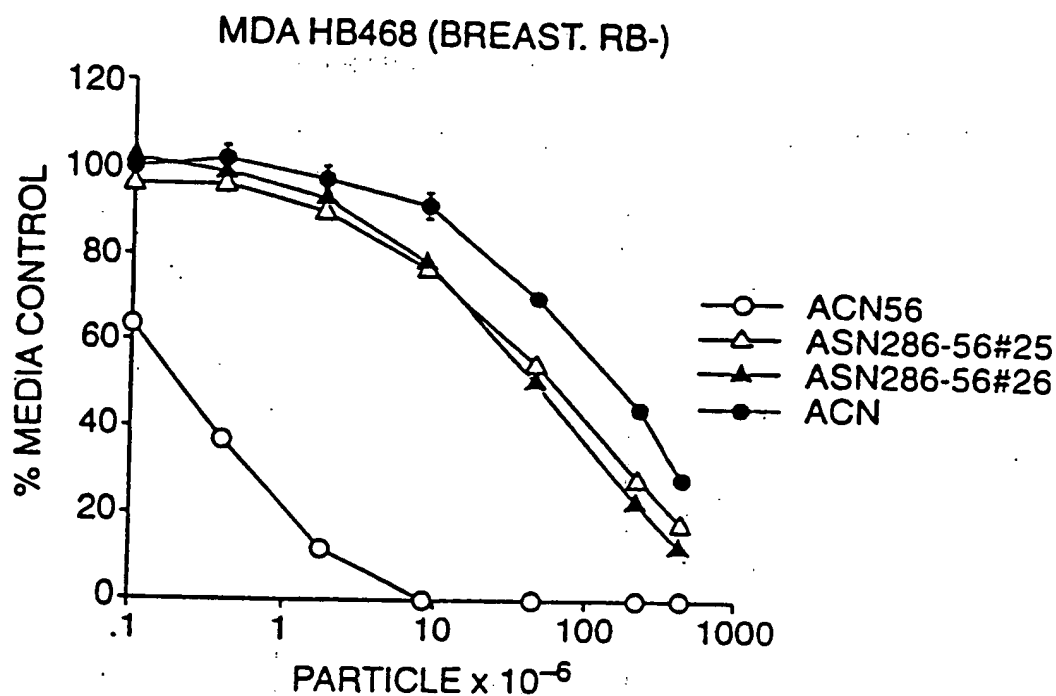


FIG. 14A

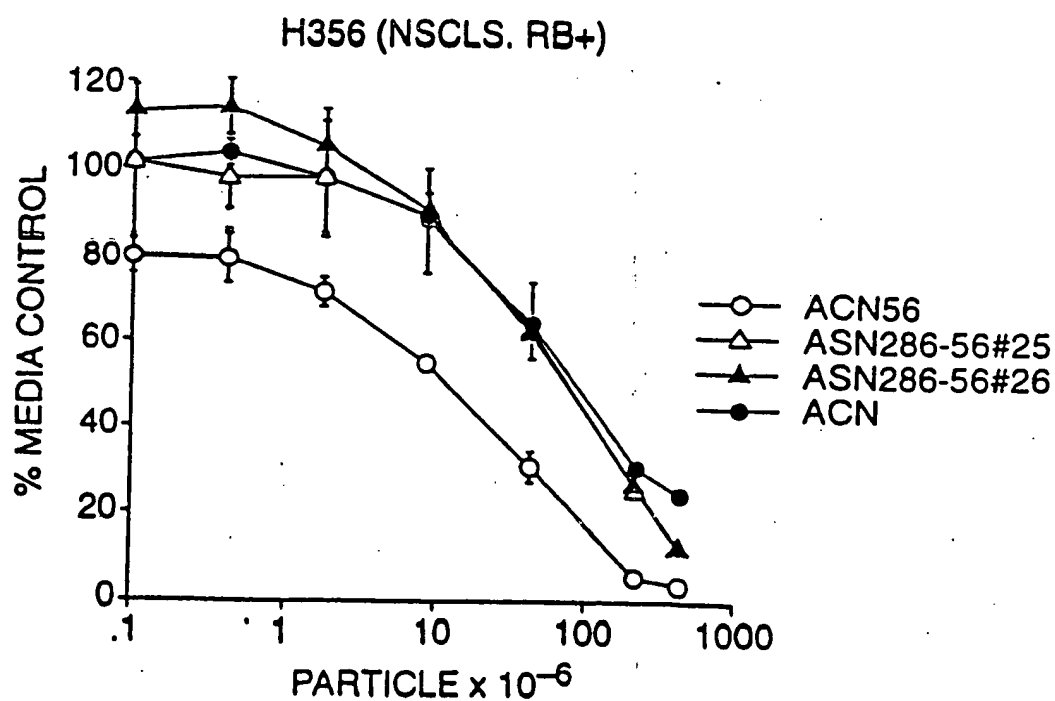


FIG. 14B



# INTIMA/MEDIA

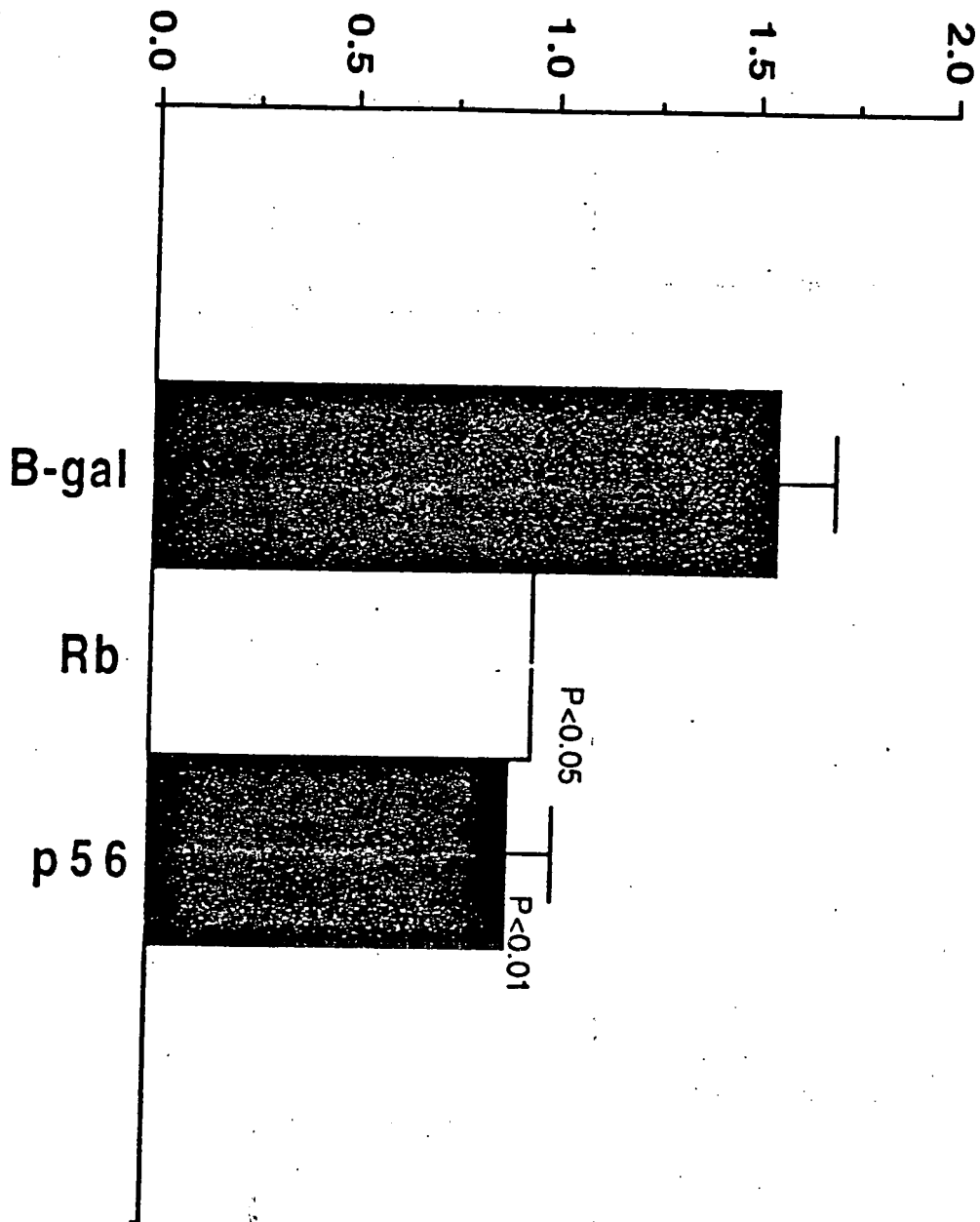


FIG. 17



A7r5 3H-THYMIDINE 83/83

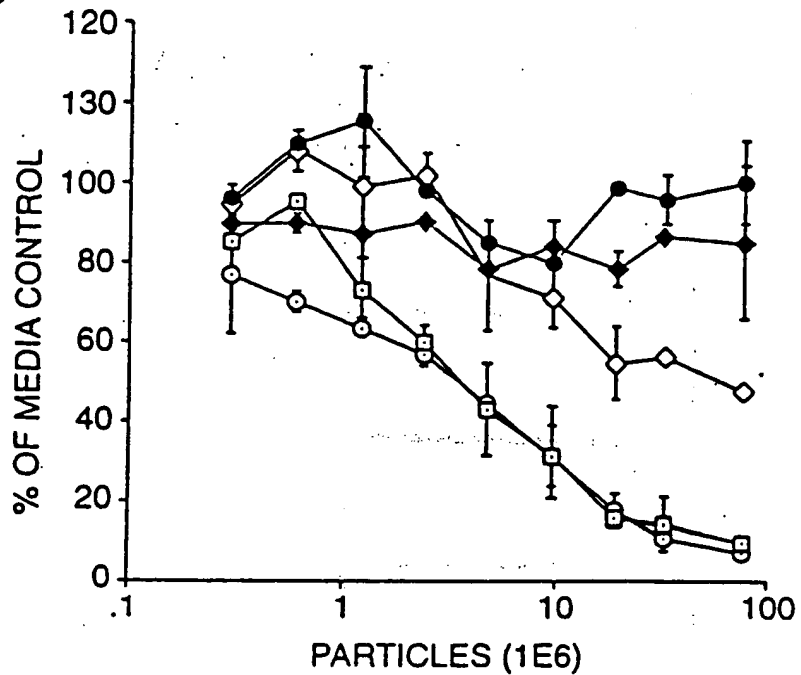


FIG. 21A

MDA468 3H-THYMIDINE

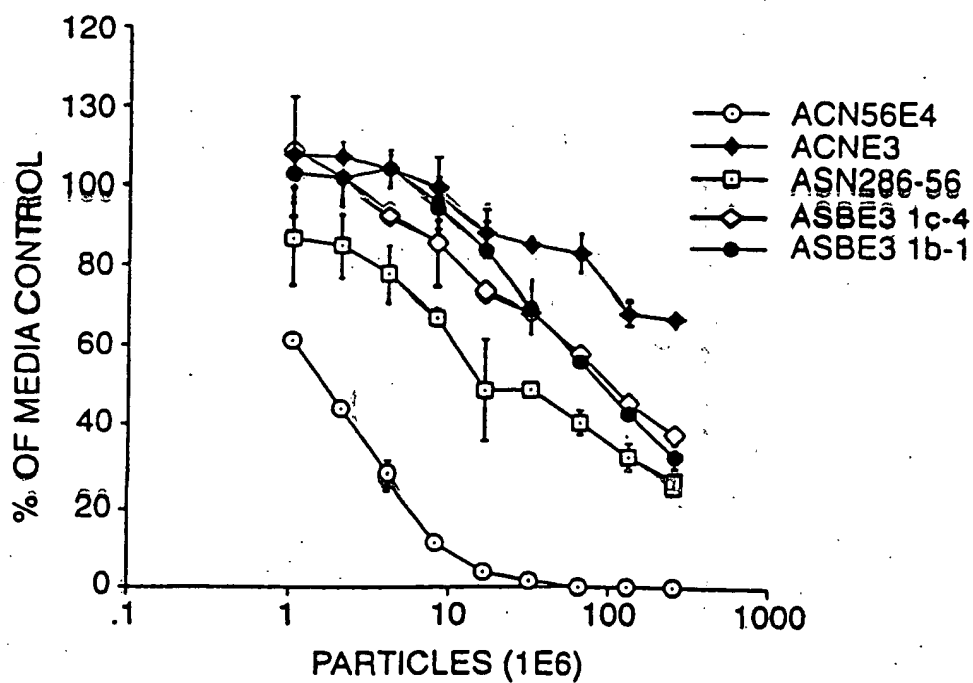
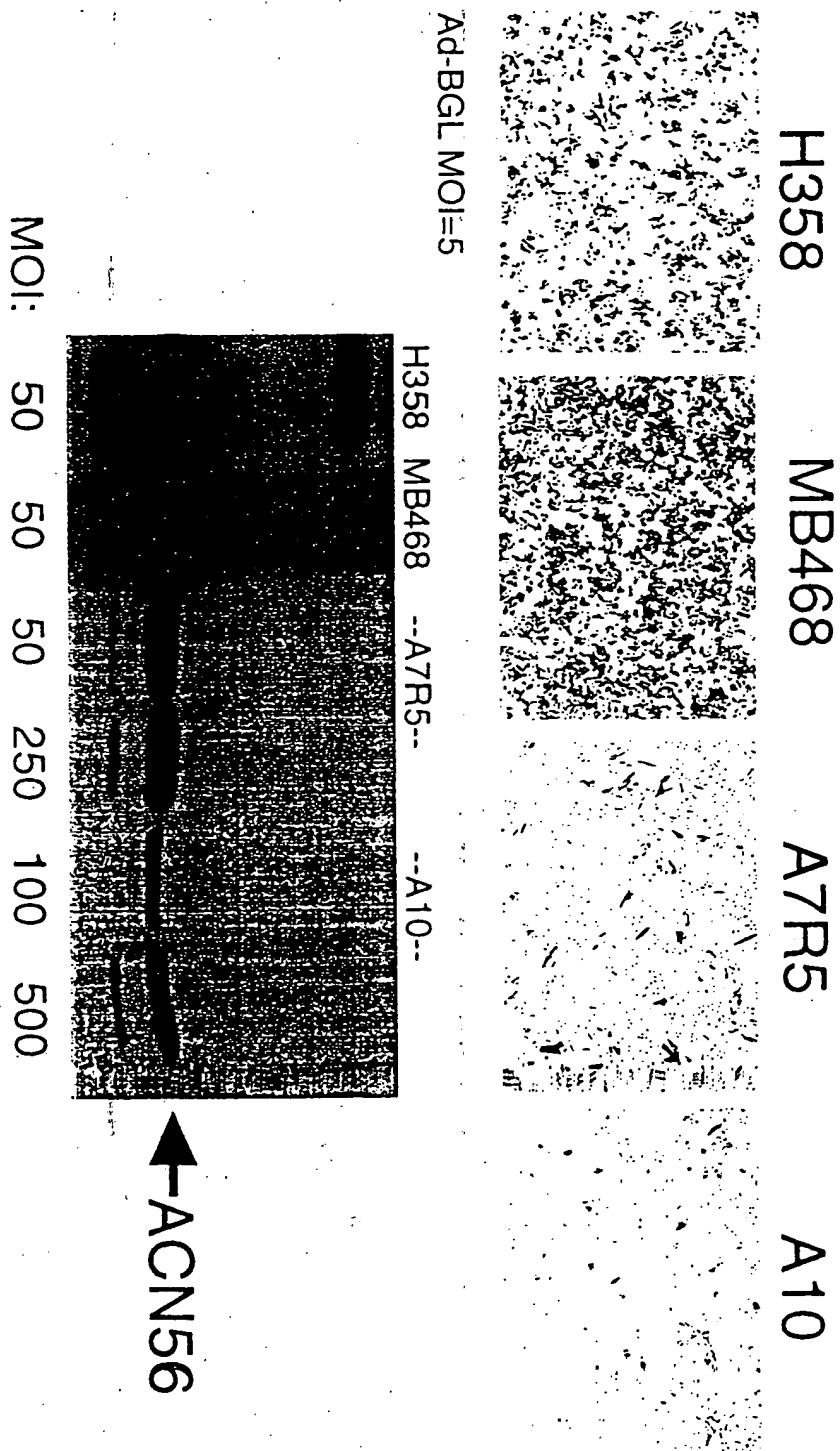


FIG. 21B



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UN 50 250 500

UN 50 250

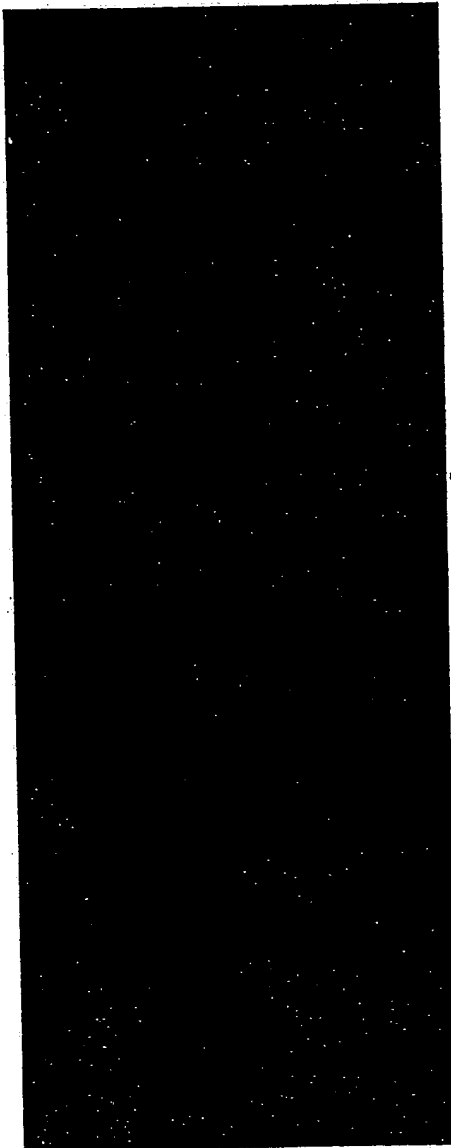
UN 100 500

**FIG. 16.**

MB468 (BREAST)

A7R5 (SM)

A10 (SM)



+

+

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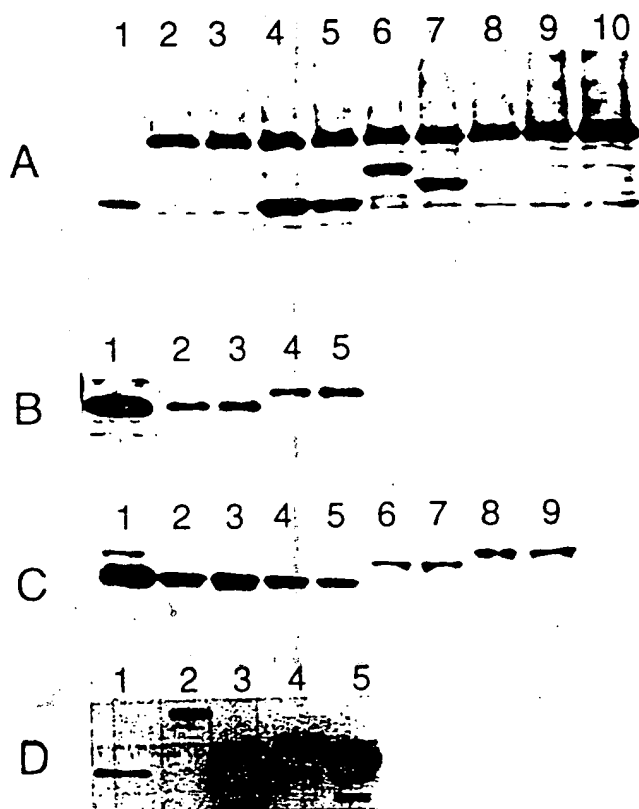


FIG. II.

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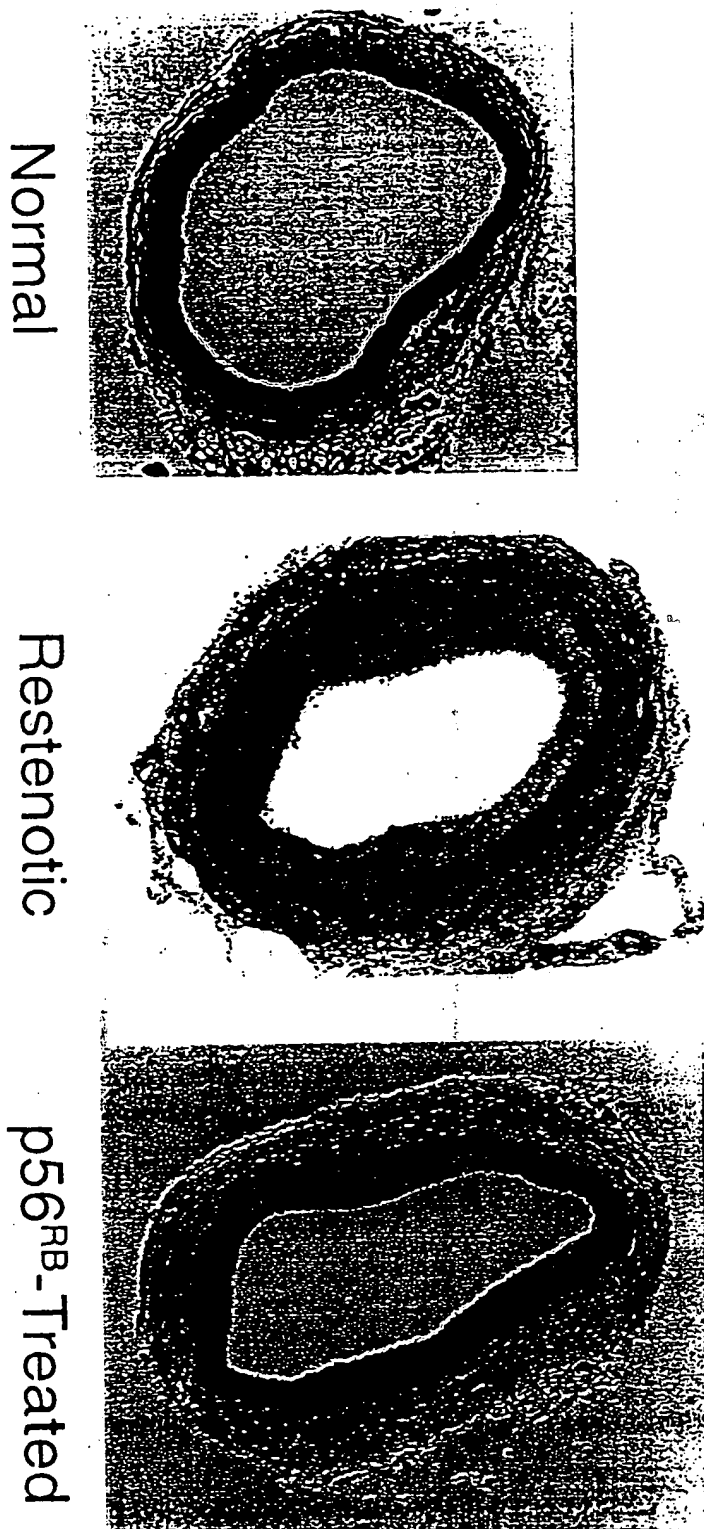


FIG. 18.



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MB468 (Breast)

MOI

A7R5 (Muscle)

ACNBGAL

1 1

ASNBGAL

100 50

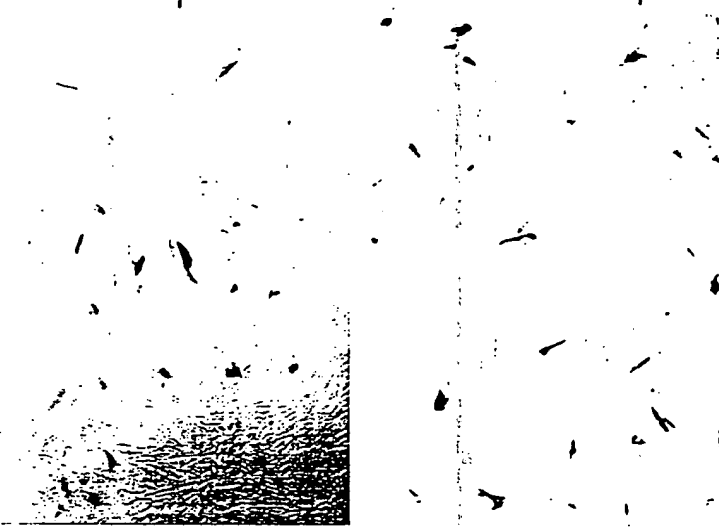
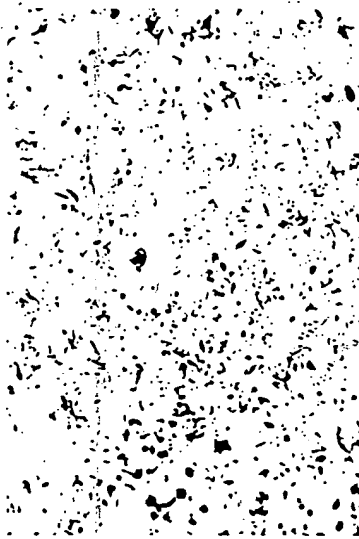


FIG. 19.



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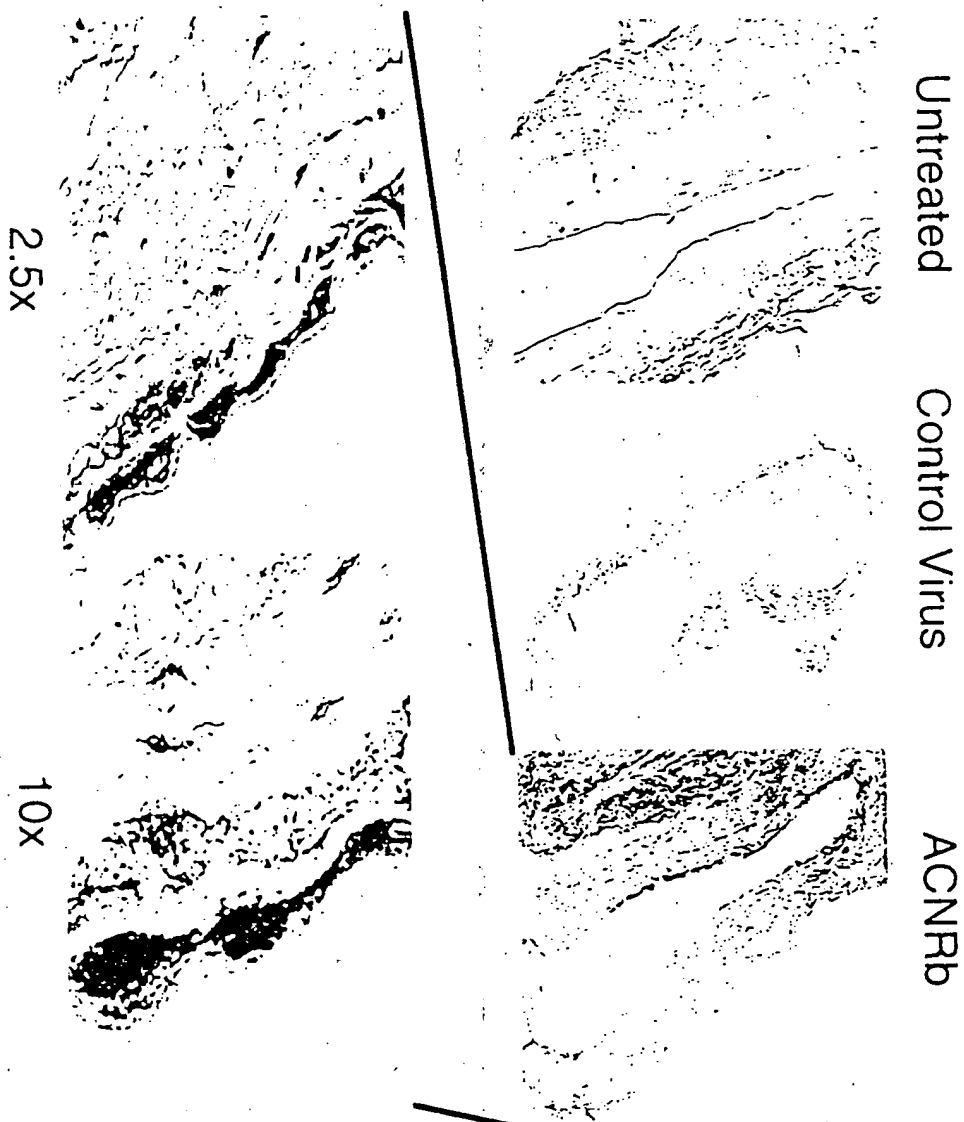


FIG. 20.

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